

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 17:33:32 ; Search time 4677.26 Seconds
(without alignments)
13261.806 Million cell updates/sec

Title: US-09-041-994-1

Perfect score: 4496

Sequence: 1 GCTGAGTGTGACTCAGAC.....CATTTGACGAGATTCTAG 4496

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13168883 seqs, 6898233199 residues

Total number of hits satisfying chosen parameters: 26337766

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	4434.2	98.6	4789	US-60-068-511-1	Sequence 1, Appl1
5	4429.6	98.5	6855	US-09-359-992-3962	Sequence 3962, Ap
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7	4421.2	98.3	7956	US-60-172-373-13551	Sequence 13551, A
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ALIGNMENTS

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US-09-041-994-1
; Sequence 1, Application US/09041994
; GENERAL INFORMATION:
;   APPLICANT: Chen, J. Don
;   APPLICANT: Li, Hui
;   TITLE OF INVENTION: Transcriptional Coactivator for Nuclear
;   TITLE OF INVENTION: Hormone Receptors
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESS: Lohive and Cockfield
;   STREET: 28 State Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02109
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/041,994
;   FILING DATE:
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Liepmann, W. Hugo
;   REGISTRATION NUMBER: 20,407
;   REFERENCE/DOCKET NUMBER: UMN-026-1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-227-7400
;   TELEFAX: 617-742-4214
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 4496 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 86..4338
;
; US-09-041-994-1
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; Query Match      100.0%; Score 4496; DB 14; Length 4496;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 4496; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT      2
US-09-513-066-1
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: Sequence 1, Application US/09513066
: GENERAL INFORMATION:
: APPLICANT: Chen, J. Don
: APPLICANT: Leo, Christopher
: APPLICANT: Li, Hui
: TITLE OF INVENTION: NOVEL USES FOR THE RAC3 TRANSCRIPTIONAL COACTIVATOR OF
: TITLE OF INVENTION: STEROID NUCLEAR RECEPTORS
: FILE REFERENCE: UMG-026CP
: CURRENT APPLICATION NUMBER: US/09/513, 066
: CURRENT FILING DATE: 2000-02-24

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1  PRIOR APPLICATION NUMBER: USSN 09/041,994
2
3  PRIOR FILING DATE: 1998-03-13
4
5  PRIOR APPLICATION NUMBER: USSN 60/073,674
6
7  PRIOR FILING DATE: 1998-02-04
8
9  NUMBER OF SEQ ID NOS: 37
10
11 SOFTWARE: PatentIn Ver. 2.0
12
13 SEQ ID NO 1
14
15 LENGTH: 4496
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17 TYPE: DNA
18
19 ORGANISM: Homo sapiens
20
21 FEATURE:
22
23 NAME/KEY: CDS
24
25 LOCATION: (86)..(4330)
26
27 OS-09-513-066-1

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Query Match	100.0%	Score 4494.4	DB 19	Length 4436
Best Local Similarity	100.0%	Pred. NC. 0		
Matches 4495	0	Mismatches	1	Indels 0
				Gaps 0

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Db 1321 gagcagacaggtctatgctgttgcagaccttagcacacagggcagatgagtgagagctag 1380
Qy 1381 GTATGGGGGTTCCAGTATACATAGCTTCAATGACCCCTGGGCCAGCATGCAATCACCATC 1440
Db 1381 gtaagggggttccagtaatacagtaagcttcaatgacccctgggcccagatgcaataccacatc 1440
Qy 1441 TTCTCTACAGAAACAACTATGGGTCACATGAGTAGGCCCCCATATGGAGTCTCG 1500
Db 1441 ttctctacagaaacaaactatgggctcacatgagtaggcccccatatggagtgctcgcg 1500
Qy 1501 TCTTGCCCCAAACACAGACAGATATCATGATTTCTCTCTGTAATGTTGGAGTCCAAAGAT 1560
Db 1501 tcttgccccaaacacagacagataatcatgattctctcgttaatcgttggaggtccaaagat 1560
Qy 1561 AGGCTACATCACTATTTTCTCTGTGAGGTGTGACATCTCCATGACATCTTGTGGCAA 1620
Db 1561 aggctacatcaactttctctgttgcaggtgtgcaactctcccatgtgcatcttcttgcaaa 1620
Qy 1621 TACTGGGAACCAAGCTTTTCCAGAGCTCTCAGTGCCTCTCAAGCCATTCAGTGAAG 1680
Db 1621 tactgggaaccaaagcttttccagagctctctcagtgccctgcaagccatccagtgaaag 1680
Qy 1681 TGTGGGACTTCCCTTTATCTACTGTGTCATCAGCAGGCCCCAAATTGATTAATCTTCC 1740
Db 1681 tgtgggacttcccttttattactactctgtcatcacaggccccaaattgataactcttc 1740
Qy 1741 CAATATGAATATTAACCAACCAAGTAAAGTAAACATCAGAGATTCCAAGAGTCTCTGGG 1800
Db 1741 caataatgaatatttaaccaaacaagtaaaagtaaaagtaaaagtaaaagtaaaagtaaaag 1800
Qy 1801 CTTTATTTGAGCAAAATCCAGTGAAGTGAATGATGCTCAATATGACAGAGATCA 1860
Db 1801 ctttatttggacaaaatccagtgagaggttcaaatgtgtcgaatcaaatagcagagatca 1860
Qy 1861 CCTCACTGACAAAGAAAGTAAAGAGAGCACTGTTGAGGGGGCAGAGAAATCAAGGGGTC 1920
Db 1861 cctcagtgaacaaagaagtaagagagcaagtgttggaggggcagagaaatcaaaagggctcc 1920
Qy 1921 TTTGGAAAGCAAGGTCATTAATAAATTACTGCAAGTTACTTACTCTGTTCTTGATGACCG 1980
Db 1921 ttggaaagcaaggtcatataaataattactgcaagttacttactactcttcttctgtgacgg 1980
Qy 1981 GGSTCAATTCCTCTTACCAACCAATCCGCCCTAGATTTCAAGTGTGAAGAAATCTTGTAG 2040
Db 1981 ggstcaatctctcttgaaccaaactccccctagattcaagtgttaagaatcttctgttag 2040
Qy 2041 TGTACACAGCCCTCTGGAGTCTCTCTCTATCTGAGAGATATCTCATATCAATCA 2100
Db 2041 tgtacacagccctctggaggtctctctctctatctgacaaagcttgcacaaagcttgcacaa 2100
Qy 2101 TATGATGGGTCACTGTATACAGAGACACCGGATTTTGACAAAGTGTGTCAGAAATG 2160
Db 2101 tatgattgggtcactgttatacagagacacccggatttttgacaaagtgtctgcagaatgg 2160
Qy 2161 GAATTCACAGCTGAGGTAGCCAAAGATTACTGCACAAGCCACTGGGAAAGACACAGAG 2220
Db 2161 gaattcacagctgaggttagccaaagattactgacaaagccactgggaaagacacacagcg 2220
Qy 2221 TATTAATCTTGTGGGAGCGAAATGTTGTCAAGACAGAGACAGTAACTTAAGAAAG 2280
Db 2221 tataacttcttggggagcgaaatgtgtcaagcaagagcaagctaaagtccctaagaagaa 2280
Qy 2281 GGAATATATGCATTTCTTATGATACCTGCTGACAGGAGATGATCTAGTATGATCTTC 2340
Db 2281 ggaaatataatgcatttcttattgatacctgtcgtgcaagggatgatactgatactgacatc 2340
Qy 2341 TAAAGAACTACAGCCCAAGTGAAGAGAGTGAATTAATATGATGACAGCAGCTC 2400
Db 2341 taaagaactacagcccaagtggaagagatggaacaataaagtaagtcagtgaccagctc 2400
Qy 2401 CACCAATTCCTAGCTCAAGTCAAGAGAAAGACCTAAATTTAAGACAGAGCAAGTAAAG 2460
Db 2401 caccattctctagctcaagtaagtaagaagaagccctaaatlaagacagagagcaagtgaa 2460
Qy 2461 GGGATCTGGAGACTTGGATATATCTAGATGCTATTTGGTGAATCTGATAGTTCTGACTT 2520
Db 2461 gggatctggagacttggatataatctagatctatcttctgtgagatctgactagttcgaact 2520
Qy 2521 TTACAATTAATTCATATCCCAATGATAGTATCTGAGGAGCTTAACCAACAGGTGTTCA 2580
Db 2521 ttacaatataatccatatctcccaatggttagtcatctcggggactcaagcaaggtgttca 2580
Qy 2581 AGGAACATAATTCCTGGGTTGAAAAGTTCAAGTCTGTGACGTATTTGCTCTCAT 2640
Db 2581 aggaactaattctctgtggtttgaaaagttcacagctcgtgcagttcatctgtctccata 2640
Qy 2641 TAACCGAGAGTGTCTGTGATAGCCCTGTTTGTGTTGGTCAAGTCTTCCATTAATAAAA 2700
Db 2641 taacgagagtggtctgtgatatagccctgttctgttggctcaagctccacgtlaaaaaa 2700
Qy 2701 TATCAGTGTCTTCCCATGTATACCAAAAGCAACCATGTTGGTGGAGATTCAGAAATGAT 2760
Db 2701 tatcagtgcttcccatcagttaccaaagaacacacagttggtggtggaatcacaagaatgat 2760
Qy 2761 GGAATAGTCAAGAAATTAATGCTCAAGTATGAGTGGGCCAAACCAAGTGAATGATGAC 2820
Db 2761 ggaatagtcagaaatatatgtctcaagtatggttgggcccacacgaatgtgactgtgac 2820
Qy 2821 TCAGACTCTTCTCTCAAGAACTGAGGCTTACCAAACTCAAAAGCCGCGCAATGGAAC 2880
Db 2821 tcagactcttctctcaggaagctggtgttcaaaaactcaaaagccggcagaaatggaacc 2880
Qy 2881 TATGAATTAATTCATGGAAGACAGAGAGAGATTAATTAATCTTTTATCCAGAC 2940
Db 2881 tatgaattcaaatctcatggaagacacagagagagatataataactcttaccacagacc 2940
Qy 2941 TGCATGGGTGCTGTATTCACATTTGCTCTGCTTAATAGACATACAGGTGCGAG 3000
Db 2941 tgcattgggtgctgtatcttccacattgctctcgtgtcaatagataccaggtgcag 3000

RESULT 4
US-60-068-511-1
; Sequence 1, Application US/60068511
; GENERAL INFORMATION:

APPLICANT: Suen, Chen-Shian
APPLICANT: Fraill, Donald E.
APPLICANT: Lytle, Richard C.
TITLE OF INVENTION: Cloning and Expression of a Nuclear
TITLE OF INVENTION: Receptor Coactivator Proteins and Uses Thereof
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/068,511
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: 97243-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-683-2169
TELEFAX: 973-683-4117
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4789 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 185..4750
US-60-068-511-1

Query Match 98.6%; Score 4434.2; DB 38; Length 4789;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 4483; Conservative 0; Mismatches 8; Indels 24; Gaps 2;
QY 1 GCTGATGCTGACCTAGAGACCAATTAATAAATTAACCTGCTTGAACATCCTTGACTGTT 60
DB 100 GCTGATGCTGACCTAGAGACCAATTAATAAATTAACCTGCTTGAACATCCTTGACTGTT 159
QY 61 AGCAATGCTGATATATATTCAGATGAGTATGAGGAAAGAACTTGGATTCACCTGCG 120
DB 160 AGCAATGCTGATATATATTCAGATGAGTATGAGGAAAGAACTTGGATTCACCTGCG 219
QY 121 CAGTATTCACGAAACGCAAAATTCGATGATCTCCAGACAGAGCTTCTACCTGCG 180
DB 220 CAGTATTCACGAAACGCAAAATTCGATGATCTCCAGACAGAGCTTCTACCTGCG 279
QY 181 TGGTGAACACGAGACGAGAGCAAGTAATATATTTGAAGATTTGGCTGAGCTGAT 240
DB 280 TGGTGAACACGAGACGAGAGCAAGTAATATATTTGAAGATTTGGCTGAGCTGAT 339
QY 241 ATCTGCATCTTATGATATTTGACATTTTCATGTCACCAACGATTAATTCGCAATTTT 300
DB 340 ATCTGCATCTTATGATATTTGACATTTTCATGTCACCAACGATTAATTCGCAATTTT 399
QY 301 AAAGAAACAGTAAAGACAGATAGTCAATTAAGAGCAAGAAAGCAATATTTCCATATG 360
DB 400 AAAGAAACAGTAAAGACAGATAGTCAATTAAGAGCAAGAAAGCAATATTTCCATATG 459

QY 361 TGATGATGTTCAAAAAGCCGATGATCTTACAGGGCAGGAGTATGATAAGACTC 420
DB 460 TGATGATGTTCAAAAAGCCGATGATCTTACAGGGCAGGAGTATGATAAGACTC 519
QY 421 CTTAGACCGCTTTTACTTCAGGCATGAGTGGTCTCTATTTGTGTGTAATGAGAGCG 480
DB 520 CTTAGACCGCTTTTACTTCAGGCATGAGTGGTCTCTATTTGTGTGTAATGAGAGCG 579
QY 481 AAACATTTGATTTGATGCAAAAATGTCACAAATCTCGCAATATTAACCAAGAGACT 540
DB 580 AAACATTTGATTTGATGCAAAAATGTCACAAATCTCGCAATATTAACCAAGAGACT 639
QY 541 GGTAAACACAGCTTTTAAATATCTTACATGAAGACACAAAGAGATTTCTTAAGA 600
DB 640 GGTAAACACAGCTTTTAAATATCTTACATGAAGACACAAAGAGATTTCTTAAGA 699
QY 601 TTTACCAAAATCTACAGTTAATGAGATTTCTGACAAATGAGCCCAACCAAAAAG 660
DB 700 TTTACCAAAATCTACAGTTAATGAGATTTCTGACAAATGAGCCCAACCAAAAAG 759
QY 661 CCATACATTTTAATGCGGTATGTTGATGAACACACATGATATTTCTGAAGACATAA 720
DB 760 CCATACATTTTAATGCGGTATGTTGATGAACACACATGATATTTCTGAAGACATAA 819
QY 721 CGCCAGTCCGAAATGCGCCAGATATGAACCAATGAGCTGTTGCCCTGCTCAGCC 780
DB 820 CGCCAGTCCGAAATGCGCCAGATATGAACCAATGAGCTGTTGCCCTGCTCAGCC 879
QY 781 ACAGCTATGATGAGAGAGGAGGAAATTTGCAATCTGTATGATCTGTGCGACGCC 840
DB 880 ACAGCTATGATGAGAGAGGAGGAAATTTGCAATCTGTATGATCTGTGCGACGCC 939
QY 841 CATTTACAGAGAGAAACATTTCCATCAAACTGAGAGCTTATTTACAGACATGA 900
DB 940 CATTTACAGAGAGAAACATTTCCATCAAACTGAGAGCTTATTTACAGACATGA 999
QY 901 TCTTTAGAAAGGTTGCAATATATGATCAAAATTCAGAGATCTCCATGAGGCTCG 960
DB 1000 TCTTTAGAAAGGTTGCAATATATGATCAAAATTCAGAGATCTCCATGAGGCTCG 1059
QY 961 CTTTGAAGATATATCGAAGGTATTCAGAGATTTTATGCTAATATGATGGCAGTC 1020
DB 1060 CTTTGAAGATATATCGAAGGTATTCAGAGATTTTATGCTAATATGATGGCAGTC 1119
QY 1021 ATGTTCCAGAAACGTCACATATCAAGACCTTATCTTAAATGGCCATGAGAAACCCAGT 1080
DB 1120 ATGTTCCAGAAACGTCACATATCAAGACCTTATCTTAAATGGCCATGAGAAACCCAGT 1179
QY 1081 ATATCATTTCTGTTGGCTGATGGAACCTATAGTACTGCACAGACAAAAGCAACTCTT 1140
DB 1180 ATATCATTTCTGTTGGCTGATGGAACCTATAGTACTGCACAGACAAAAGCAACTCTT 1239
QY 1141 CCGAAATCTGTACAAATGATGACATGGCTTTGCTCAACCCATCTCTCAGAGAGA 1200
DB 1240 CCGAAATCTGTACAAATGATGACATGGCTTTGCTCAACCCATCTCTCAGAGAGA 1299
QY 1201 ACAGATGATATAGACCAAAACCAATCTGTTGGACAAAGGATTAACCACTATGCG 1260
DB 1300 ACAGATGATATAGACCAAAACCAATCTGTTGGACAAAGGATTAACCACTATGCG 1359
QY 1261 TGGATCAACAGTTCGGTGGGCGCATGAGTATGTGCCAACAAGCTTACAGATGCC 1320
DB 1360 TGGATCAACAGTTCGGTGGGCGCATGAGTATGTGCCAACAAGCTTACAGATGCC 1419
QY 1321 GAGCAGCAGGCGCTATGGCTGAGACACCTAGCACAGGCGAATAGTGGAGCTAG 1380
DB 1420 GAGCAGCAGGCGCTATGGCTGAGACACCTAGCACAGGCGAATAGTGGAGCTAG 1479
QY 1381 GTATGGGGGTTCCAGTAAATAGCTTCAATTTGACCCCTGGGCCAGGAGTCAATCAACATC 1440
DB 1480 GTATGGGGGTTCCAGTAAATAGCTTCAATTTGACCCCTGGGCCAGGAGTCAATCAACATC 1539

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Db 1540 TTCTACCAAGAACAACTATGGGCTCAACATGATAGTACCCCAACATGGAGTCTGG 1599
1501 TCTTCCCCAAACAGCAAGATATCATGATTTCTCTCGTAATGCGGGAGTCCAAAGAT 1560
1600 TCTTCCCCAAACAGCAAGATATCATGATTTCTCTCGTAATGCGGGAGTCCAAAGAT 1659
1561 AGCCTACATCATGTTTCTCTGAGTGTGACACTCTCCATGGCATCTTCTGGCA 1620
1660 AGCCTACATCATGTTTCTCTGAGTGTGACACTCTCCATGGCATCTTCTGGCA 1719
1621 TACTGGGAACCAAGCACTTTTCCAGAGCTCTCTCACTGCGCTCCGAAGCATAGTGAAG 1680
1720 TACTGGGAACCAAGCACTTTTCCAGAGCTCTCTCACTGCGCTCCGAAGCATAGTGAAG 1779
1681 TGTGGGAGCTTCCCTTTTATCTACTCTGTGATCACCAGAGCCCAATTGGATACCTCC 1740
1780 TGTGGGAGCTTCCCTTTTATCTACTCTGTGATCACCAGAGCCCAATTGGATACCTCC 1839
1741 CAATATGAATATTTACCAACCAAGTAAAGTAAGCAATCAGATTTCCAAAGTCTCTGGG 1800
1840 CAATATGAATATTTACCAACCAAGTAAAGTAAGCAATCAGATTTCCAAAGTCTCTGGG 1899
1801 CTTTATTTGGCCAAATTCAGTGGAGAGTTCAATGTGTGATCAATATAGCAGATCA 1860
1900 CTTTATTTGGCCAAATTCAGTGGAGAGTTCAATGTGTGATCAATATAGCAGATCA 1959
1861 CCTCAGTACAAAGAAATTAAGAGAGAGTGTGAGGGGCGAGAAATCAAGAGGCTCC 1920
1960 CCTCAGTACAAAGAAATTAAGAGAGAGTGTGAGGGGCGAGAAATCAAGAGGCTCC 2019
1921 TTTGGAAGCAAAAGTCAATAAAAAATTACTGAGTTACTTACTCTTCTTGATGACCG 1980
2020 TTTGGAAGCAAAAGTCAATAAAAAATTACTGAGTTACTTACTCTTCTTGATGACCG 2079
1981 GGGTATTCCTCTTACCAACTCCCTCTAGATTCAGTTGTAAGAAATCTCTGTAG 2040
2080 GGGTATTCCTCTTACCAACTCCCTCTAGATTCAGTTGTAAGAAATCTCTGTAG 2139
2041 TGTCAACGAGCCCTCTGAGTCTCTCTCAATCTGGAGAGTATCTCTACATCCAA 2100
2140 TGTCAACGAGCCCTCTGAGTCTCTCTCAATCTGGAGAGTATCTCTACATCCAA 2199
2101 TATGATGGGTCTCTGTTTACAAAGAGACACCGGATTTTGCACAAAGTGTGACAAATGG 2160
2200 TATGATGGGTCTCTGTTTACAAAGAGACACCGGATTTTGCACAAAGTGTGACAAATGG 2259
2161 GAATTCACAGCTGAGTAGCCAAAGATTACTGCAACAGCACTGGGAAAGACACGAGAG 2220
2260 GAATTCACAGCTGAGTAGCCAAAGATTACTGCAACAGCACTGGGAAAGACACGAGAG 2319
2221 TATAAATTCTTGTGGGAGCGGAATGTTGTCAAGCAGAGCAGCTTAACTCTTAAGAGAA 2280
2320 TATAAATTCTTGTGGGAGCGGAATGTTGTCAAGCAGAGCAGCTTAACTCTTAAGAGAA 2379
2281 GGAGAAATATGACACTTCTTAAGTACTGCTGACAGGAGTATCTTACTGATGACTCTC 2340
2380 GGAGAAATATGACACTTCTTAAGTACTGCTGACAGGAGTATCTTACTGATGACTCTC 2439
2341 TAAAGAACTACAGCCCAAGTGAAGAGATGGACAAATAAATGATCAGTGCACAGCTC 2400
2440 TAAAGAACTACAGCCCAAGTGAAGAGATGGATTAATAAATGATCAGTGCACAGCTC 2499
2401 CACCAATTCCTAGCTCAAGTCAAGAGAAAGACCTTAAATTAAGACAGAGACAAAGTGAAG 2460
2500 CACCAATTCCTAGCTCAAGTCAAGAGAAAGACCTTAAATTAAGACAGAGACAAAGTGAAG 2559
2461 GGGATCTGGAAGCTTGATTAATCTAGATGCTATTTCTGGTATCTGACTAGTTCTGACTT 2520
2560 GGGATCTGGAAGCTTGATTAATCTAGATGCTATTTCTGGTATCTGACTAGTTCTGACTT 2619
2521 TTACAATAATTCATATCTCTCAAAATGATGATCATCTGGGAGCTTAAGCAAGGCTTTTCA 2580

Db 2620 TTACAATAATTCATATCTCTCAAAATGATGATCATCTGGGAGCTTAAGCAAGGCTTTTCA 2679
2581 AGCACTAATTCCTGGGTTTGAAGAGTTACAGAGCTGTGGAGTCTATTCGCTCCATA 2640
2680 AGCACTAATTCCTGGGTTTGAAGAGTTACAGAGCTGTGGAGTCTATTCGCTCCATA 2739
2641 TAACGAGAGTGTCTCTGATAGGCTGTCTGTGTTGCTCAAGTCTCCAGTAATAAAA 2700
2740 TAACGAGAGTGTCTCTGATAGGCTGTCTGTGTTGCTCAAGTCTCCAGTAATAAAA 2799
2701 TATCAGTGTCTTCCCATGTTTACCAAGCAACCCATGTTGGGTGGGAATCCAAGATATAT 2760
2800 TATCAGTGTCTTCCCATGTTTACCAAGCAACCCATGTTGGGTGGGAATCCAAGATATAT 2859
2761 GATATGTCAGGAAATTTATGCTCAAGTATGAGTGGGCAACCAAGTATGACTGTGAC 2820
2860 GATATGTCAGGAAATTTATGCTCAAGTATGAGTGGGCAACCAAGTATGACTGTGAC 2919
2821 TCAGACTCTCTCTCAGAGACTGGGGCTTACCAAACTCAAAAGCCGCGAGATGGAAC 2880
2920 TCAGACTCTCTCTCAGAGACTGGGGCTTACCAAACTCAAAAGCCGCGAGATGGAAC 2979
2881 TATGAATTCAAACTCCATGGGAAGACAGAGAGATTAATTAATCTTTTACCAGACC 2940
2980 TATGAATTCAAACTCCATGGGAAGACAGAGAGATTAATTAATCTTTTACCAGACC 3039
2941 TGCACCTGGGTCTATTTCCCATGCTCTCTGCTATATACATACAGAGTGGCAG 3000
3040 TGCACCTGGGTCTATTTCCCATGCTCTCTGCTATATACATACAGAGTGGCAG 3099
3001 ACCAGTATTCGAACAGCAGCAGAGATCTTCAATTAAGCCCTGTGTAATCCCATGGG 3060
3100 ACCAGTATTCGAACAGCAGCAGAGATCTTCAATTAAGCCCTGTGTAATCCCATGGG 3159
3061 AATGGGGCTAATCCCTTGGGCAAGCAGAGATCTTAACCACTGGGTCTGGCCCGA 3120
3160 AATGGGGCTAATCCCTTGGGCAAGCAGAGATCTTAACCACTGGGTCTGGCCCGA 3219
3121 TGGCATGTTGTCCATGGAACAAATTTCTCATGGCACTCAAAATAGGCTCTTCTTAGGA 3180
3220 TGGCATGTTGTCCATGGAACAAATTTCTCATGGCACTCAAAATAGGCTCTTCTTAGGA 3279
3181 TTCCCTGATGATCTTGTGGGCACTTCCAACTGGAAGCCAGAGTGAACAGAGC 3240
3280 TTCCCTGATGATCTTGTGGGCACTTCCAACTGGAAGCCAGAGTGAACAGAGC 3339
3241 ATTATTTGACAGCTGCACTCTTCTCAGCAACAGATGCAAGGCTTGAAGAAAT 3300
3340 ATTATTTGACAGCTGCACTCTTCTCAGCAACAGATGCAAGGCTTGAAGAAAT 3399
3301 TGACAGAGCTTTGGGATTTCTGAACTTGTCAATCAGGAGAGGATTAAGCCCAACA 3360
3400 TGACAGAGCTTTGGGATTTCTGAACTTGTCAATCAGGAGAGGATTAAGCCCAACA 3459
3361 GGATCTTTTCCAAAGGCCCAAGAGCAGTATGATGATGATGATGATGATGATGATG 3420
3460 GGATCTTTTCCAAAGGCCCAAGAGCAGTATGATGATGATGATGATGATGATGATG 3519
3421 ACAGCATACCCAGACAGGGGGCTCCAAATGCAAGGAGAGCTTATCTTCAGGGACAATC 3480
3520 ACAGCATACCCAGACAGGGGGCTCCAAATGCAAGGAGAGCTTATCTTCAGGGACAATC 3579
3481 ACCATCTTTTAACTCTATGATGAATCAGATTAACAGCAAGCAATTTTCTCTCAAGG 3540
3580 ACCATCTTTTAACTCTATGATGAATCAGATTAACAGCAAGCAATTTTCTCTCAAGG 3639
3541 AATGCAACCCAGAGCAACATCATGAGACCCCGGCAAAACACCCCAAGCAACTTAGAAT 3600
3640 AATGCAACCCAGAGCAACATCATGAGACCCCGGCAAAACACCCCAAGCAACTTAGAAT 3699
3601 GCAGCTTACAGAGAGGCTGACAGGGCCAGCACTTTTGAATACAGCCGACAGGCACTTGA 3660

Db 3700 GCAGCTTCAGAGAGGCTGAGGCGCCAGAGTTTGTGAATCAGAGCCAGGCACTTGA 3759
Oy 3661 ATTGAAATGAAAAACCTACTGCTGTGTGTGCTGGGATGAGGCTATGATGAGCC 3720
Db 3760 ATTGAAATGAAAAACCTACTGCTGTGTGTGCTGGGATGAGGCTATGATGAGCC 3819
Oy 3721 CCAG-----CAGGGTTTTCTTAATGCTCAAAATGCTGGCCAAACGAGAGAGAGCT 3771
Db 3820 CCAGGTGAGCTCCAGAGGTTTTCTTAATGCTCAAAATGCTGGCCAAACGAGAGAGAGT 3879
Oy 3772 GCTAAGTCTACTCTCCGAAACAGAGGCTGCTATGATGATGAGCAGCAGCA----- 3826
Db 3880 GCTAAGTCTACTCTCCGAAACAGAGGCTGCTATGATGATGAGCAGCAGCAGCA 3939
Oy 3827 -----CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 3876
Db 3940 GCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 3999
Oy 3877 ACAGCAGCAAAACCCAGGCTTACGCCACCTCTAATGTGACTGCTTCCCGCAGATGGA 3936
Db 4000 ACAGCAGCAAAACCCAGGCTTACGCCACCTCTAATGTGACTGCTTCCCGCAGATGGA 4059
Oy 3937 TGGGCTTTTGGCAGAGCACCACCAATGCGCAGAGCTCTCCGAAACAGTTTCCATATCAACC 3996
Db 4060 TGGGCTTTTGGCAGAGCACCACCAATGCGCAGAGCTCTCCGAAACAGTTTCCATATCAACC 4119
Oy 3997 AATTTATGAAATGGGCAACCAACAGATCCAGCTTTGGTCCAGTCTTATGCTCTCCAA 4056
Db 4120 AATTTATGAAATGGGCAACCAACAGATCCAGCTTTGGTCCAGTCTTATGCTCTCCAA 4179
Oy 4057 TGCATATGATGCTGCTCAAGATGGGTCTCTCCAGATCCCATGATGATGATGATGATGAT 4116
Db 4180 TGCATATGATGCTGCTCAAGATGGGTCTCTCCAGATCCCATGATGATGATGATGATGAT 4239
Oy 4117 TGCATATGATGCTGCTCAAGATGGGTCTCTCCAGATCCCATGATGATGATGATGATGAT 4176
Db 4240 TGCATATGATGCTGCTCAAGATGGGTCTCTCCAGATCCCATGATGATGATGATGATGAT 4299
Oy 4177 CAGCTCCCTTTCCCGCAGCAGTTCGCCACCGAGGGGATCCGCGATGATGATGATGATGAT 4236
Db 4300 CAGCTCCCTTTCCCGCAGCAGTTCGCCACCGAGGGGATCCGCGATGATGATGATGATGAT 4359
Oy 4237 GCACATGATGAGCAGAGTGTGTACATGAGCAGATGAACATGAACCCATGCCATGTC 4296
Db 4360 GCACATGATGAGCAGAGTGTGTACATGAGCAGATGAACATGAACCCATGCCATGTC 4419
Oy 4297 TGGCATGCTATGGGTCTGTATCAGAAATACCTGTGACATCTCTGACACAGAGCTCTTA 4356
Db 4420 TGGCATGCTATGGGTCTGTATCAGAAATACCTGTGACATCTCTGACACAGAGCTCTTA 4479
Oy 4357 AGGAAACCACTGTACAAATGACACTGACATAGATATTGGGAAGAAATCATTTGTTCCAG 4416
Db 4480 AGGAAACCACTGTACAAATGACACTGACATAGATATTGGGAAGAAATCATTTGTTCCAG 4539
Oy 4417 GCATCATCTTGGAAAGAAAGAGCAGCTTGGAGCTCCATCAAGAGGATTTTAAGTATGAT 4476
Db 4540 GCATCATCTTGGAAAGAAAGAGCAGCTTGGAGCTCCATCAAGAGGATTTTAAGTATGAT 4599
Oy 4477 CATTTGAGCAGGAT 4491
Db 4600 CATTTGAGCAGGACT 4614

RESULT 5

US-09-359-922-3962
; Sequence 3962, Application US/09359922
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc.
; TITLE OF INVENTION: NOVEL CONFIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/359, 922
; CURRENT FILING DATE: 1999-07-22

; EARLIER APPLICATION NUMBER: US 09/205,155
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3962
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6855)
; OTHER INFORMATION: n = A,T,C or G
US-09-359-922-3962

Query Match 98.5%; Score 4429.6; DB 17; Length 6855;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 4482; Conservat 0; Mismatches 9; Indels 27; Gaps 2;

Oy 1 GCTGATGCTGAGCTCAGAGACCAATAAATAACTGCTGACATCTTGTGAGTGT 60
Db 116 gctgatactgagctcagagacccaataaataaactgctgacatcttgcactgct 175
Oy 61 ACCAGTTCCTGATGATATTTCAAGATGATGATGATGATGATGATGATGATGATGAT 120
Db 176 agccagctgctgatactatctcaagctgagctgagctgagctgagctgagctgag 235
Oy 121 CAGTATTCAGCAAAACGCAATGCTGATGATGATGATGATGATGATGATGATGATGAT 180
Db 236 cagctatcagcaaaacgcaatgctgatactgatactgatactgatactgatactgata 295
Oy 181 TGGTGAAGAAAGGAGAGCGGAGAGCAAGTAAATATGAAATGCTGAGCTGAT 240
Db 296 tggtagaagaaaggagagcgagagcaagttaaattgaaattgctgagctgat 355
Oy 241 ATCTGCAATCTTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 356 atctgcacatctttagatgatactgatactgatactgatactgatactgatactgata 415
Oy 301 AAAGCAACAGTACAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Db 416 aaagcaaacagtacagcagatgatactgatactgatactgatactgatactgatactgata 475
Oy 361 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (184)...(4422)
US-09-440-612-1

Query Match 96.1%; Score 4322.2; DB 18; Length 6754;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 4438; Conservative 0; Mismatches 8; Indels 81; Gaps 3;

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QY 61 AGCCAGTGTGTGATATATTCAAGATGAGTGAATAGCAAACTTGATCCACTGC 120
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Db	4494	tcattgtcttcaggatcatccatctctggaagaagaccagtttgactctcatcaaggytat	4553
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RESULT 11
US-09-440-612-3
: Sequence 3, Application US/09440612A
: GENERAL INFORMATION:
: APPLICANT: C. Frank Bennett
: TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-3 EXPRESSION
: FILE REFERENCE: RTS-0042
: CURRENT APPLICATION NUMBER: US/09/440,612A
: FILING DATE: 1999-11-15
: NUMBER OF SEQ ID NOS: 49
: SEQ ID NO 3
: LENGTH: 6754
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (184)..(4422)
: US-09-440-612-3

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Query Match	96.18;	Score 4322.2;	DB 18;	Length 6754;
Best Local Similarity	98.08;	Pred. No. 0;		
Matches 4438;	Conservative	0;	Mismatches 8;	Indels 81; Gaps 3;

[illegible]


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RESULT 13
US-09-652-127-9831
; Sequence 9831, Application US/09652127
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1183-001
; CURRENT APPLICATION NUMBER: US/09/652,127
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,134
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 10475
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9831
; LENGTH: 7888
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-652-127-9831

Query Match 95.9% Score 4313 DB 25 Length 7888
Best Local Similarity 97.9% Pred. No. 0:
Matches 4436: Conservative 0: Mismatches 10: Indels 87: Gaps 3:
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RESULT 14588
US-09-652-355-11058
; Sequence 11058, Application US/09652355
; GENERAL INFORMATION:
; APPLICANT: Shytan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1192-001

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; CURRENT APPLICATION NUMBER: US/09/652,355
 ; CURRENT FILING DATE: 2000-08-30
 ; PRIOR APPLICATION NUMBER: 60/151,136
 ; PRIOR FILING DATE: 1999-08-30
 ; NUMBER OF SEQ ID NOS: 11227
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11058
 ; LENGTH: 7888
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-652-355-11058

Query Match 95.9%; Score 4313; DB 25; Length 7888;
 Best Local Similarity 97.9%; Pred. NO. 0;
 Matches 4436; Conservative 0; Mismatches 10; Indels 87; Gaps 3;

QY 1 GGTGATGATGACACGACGACCAATTAATAAATGCTGTGAACATCTTGTGACGTT 60
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 Db 97 gctgagatggtgactcgaagacccaataaataaactctgtaacatccttgactggtt 156
 QY 61 AGCCAGTTGCTGATGATATTCAGATGAGTGTAGAGAAAATTGATCCACTGCG 120
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 Db 157 agccagttgctgactgatactcgaagatggtgtatgagagaacttgatccactgyc 216
 QY 121 CAGTGATTCAGCAAAACGCAATTTGCCATGTGATCTCCAGACAAAGTCTTACCTGCAG 180
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 Db 217 cagtgatcagcaaaacgcaaaatgcacatgatactccagagcaggtcttaacctgcag 276
 QY 181 TGGTGAAGAAAGGAGAGCGGAGCAGAGAAATTAATATTGAAGATTGGCTGAGCTGAT 240
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 Db 277 tgggtgaagaaagagagcagagagcaagataataatactgaaagatcggcagagctgac 336
 QY 241 ATCTGCCAATCTTGTGATGATGACATTTCAATGTCAACACGATGAATGTCGATTTT 300
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 Db 337 atctgccaatcttgtgatactgacaatttcaatgtaacccaagataatgtgcgatttt 396
 QY 301 AAAGCAACAGTAAGACAGATACGTCATTAATAAAGCAAGAAAACATTTTCCATTA 360
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 Db 397 aaagcaaacagtaagacagatacgtcaaaataaagagcaagaaaactatctccatg 456
 QY 361 TGATGATGTTCAAAAAGCCGATGTAATCTCTACAGGGGCGGAGTTATGATTAAGATC 420
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 Db 457 tgatgattgtcaaaaagccgagatctcttcacagagagagatattgataaaaccc 516
 QY 421 CTTAGACCGCTTTTACTTCAGGCAATGAGTGTGTTCTATTGTGCTGAATCGAGCGC 480
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 Db 517 cttagaccgcttttacttcagcatggaigtcttcctatttggtgtaactcgagacg 576
 QY 481 AAACATTTGATTTGTTTCAAAAATGTCAACATTAATCTGCAATATTAACAAGAGACCT 540
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 Db 577 aaacattgatttctgtacagaaaatgtcacacaatacctgcaataataagcaagagac 636
 QY 541 GGTTAACAAGATGTTTACAAATATCTTACATGAAGAAGACAGAAAGATTTCTTAAGA 600
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 Db 637 ggttaacaagatggttttaacaatacttacaagaagaagcaagaagatttcttaagaa 696
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 Db 697 tttaaccaaaatctacagtttaactgaggtttccctgacaaatgagcccaagaacaaaag 756
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 Db 757 ccatacatttaatgcccgaatgtgtgaataaacacacacataatcttgaaagacataaa 816
 QY 721 CCGCAGTCCTGAATGCGCAGAGATATGAACAATGACGTCTTGGCCTGTCTCAGCC 780
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 Db 817 ccgcagtcctgaataatgcccagagatataaacaatgacagtgcttgcctccctcagacc 876
 QY 781 AGGACCTATGATGAGGAAGGGAAGATTGCAATCTTGTATGATCTGTGGACGCCG 840
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 Db 877 acgagctatgatgaggaaggggaagattctgcaatcttgtatgactgtgtgagcagccg 936

QY 841 CATTTACTACAGAGAAAGACATTTTCATCAAAACCTGAGACCTTTATTACGACATGA 900
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 QY 1021 ATGTCCAGAAAGCTCACTATCAAGA-----AGC 1050
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 Db 1117 atgtccagaaagctcactactcaagaagtacacagtgatgagatatttcccaacagc 1176
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 Db 1297 cttgtcttaacccacttcttcagagagaacagatgataatgacaaacccaatcc 1356
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 Db 1417 tatgtgccaaaccaaaggtttacagatgagcagcagcagcagctatgcttgagacacc 1476
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 Db 1597 catgagtagcccccaacatgagatctgtcttgcaccaaacagcagaataatcatgat 1656
 QY 1531 TTTCTCTGCTAATCGTGGAGATGCCAAAGATACGCTACATCATGTTTCTCTGTTGACAG 1590
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 Db 1657 ttctctcgttaacgtgagagatccaaagataagcctcaactcagtttctcctgttgcag 1716
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 Db 1717 tgtgcaacttcccataggaatctcttcggaataatcttggaacacacagcttctccagagctc 1776
 QY 1651 TCTCAGTGCCTGCAAGCCATCATGATGAAGTGTGGGACTTCCCTTTATCTCTGTC 1710
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 Db 1777 tctcagtgccctgcaagcccatcagtgaaagtgtgggagcttcccttatactacactgttc 1836
 QY 1711 ATCACCAGGCCCAAAATGGAATCTCCCAATTAATGAATATTACCAACCAAGTAATGT 1770
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 Db 1837 atcacagagccccaatttgaataactctcccaatagatatacttaccacaacgaagtaagt 1896
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 Db 1897 aagcaatcagagttccaaagatctcttgaggcttatacttgagccaaatccagtgagag 1956
 QY 1831 TTTCAATGTGTCAATTAAGCAAGATCACCTCAGTGAACAAAGATTAAGAGAGAG 1890
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 Db 1957 ttcaatgtgtcgaataatagagatacactcagtgacaagaagtaagagagagcag 2016
 QY 1891 TGTGAGGGGGCAGAGATCAAAAGGGTCTTTGGAAAAGCAAGGTCAATAAAATTTACT 1950

Qy	4099	GATGCAACACCCCGAGGCTGCATCCATCTATCATAGTCTCTGAAATGAAGGCTGGCCATC	4158
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Qy	4159	AGGAAATTTGGCCGGAAACAGTCCTTTTCCGAGCGAGTTTGGCCACCAAGGGGAATCC	4218
Db	4232	aggaaatcttggccaggaaacagctccctcttcccgcgcagcttgcaccacagggaaacc	4311
Qy	4219	TGCAGTGTATAGTATGGTCACATGATGATGGACAGCAATGGTCACATGGAGACAGATGAACAT	4278
Db	4312	tgcagtgatagtaigtgtgacatgaaatgagcagtgctacatcgtggacagatgaataat	4371
Qy	4279	GAACCCCATGCCATCTGTCTGGCATGECCTATGGTCTCTATCAAGAAATCTGCTGCATCT	4338
Db	4372	gaaccccatgcccatctgtcttgcctatgctcctatggctctgacaaatctactctgaatcct	4431
Qy	4339	CTGCACACGAGACCTTTAAAGAAACACAGTGCACATGACATGACATAGGATTAATTTGG	4398
Db	4432	ctgcacaagacctcttaagaaacaacgtlaaanaatgacaatctgacatcagaattatgg	4491
Qy	4399	AAGGAATCATTTGTTCCAGGATCCATCTTGGAAGAAAGACAGCTTTGAGCTCCATCAA	4458
Db	4492	aaggaaatcatctgttccagatcatcattcttgaagaaggaacagctttagctctcatcaa	4551
Qy	4459	GGGTATTTTAAGTGTATCTCTTTGACGAGAAAT	4491
Db	4552	gggtatcttaagtgtatctcttcttgaacaggaact	4584

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RESULT 15
US-09-663-1028
; Sequence 1028, Application US/09663693
; GENERAL INFORMATION:
; APPLICANT: Geirling, David P.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1195-001
; CURRENT APPLICATION NUMBER: US/09/663,693
; CURRENT FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/154,986
; PRIOR FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 1340
; SOFTWARE: Fastseq for Windows Version 4.0
; SEQ ID NO 1028
; LENGTH: 7888
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-663-693-1028

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	Query Match	Similarity	95.98%	Score 4213	DB 26	Length 7888	
	Best Local	Similarity	97.98%	Pred. No. 0			
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Db	97	gctgtagtggtagctccagagaccataaaaaaaactgcttgaacctcttgactcgtgt	156				
Qy	61	AGCCAGTTCGCTGATGTATATTCAAGATGAGTGATTTAGAGAAAACCTTGATCCACTGGC	120				
Db	157	agccagctgctgactatcatcagaatggtgattagagaanaacttgatccacttgc	216				
Qy	121	CAGTGATTCACGAAAACGCAAAATTGGCATGTGTATCTCCAGGCAACAGTCTTACTCTGCAG	180				
Db	217	cagtgattccagaaaacgcaaaatgcccagtgtactccaggaacaagctcttaccctgcag	276				
Qy	181	TGGTGAAAAACCGAGACGGGAGCAGAGAAAGTAAATATTATTTGAAGAAATTGGCTGACGTGAT	240				
Db	277	tggtagaaaaacggagacggggagccaggaagttaaatattgaagaacttgcctggaagctgat	336				
Qy	241	ATCTCCCAATCTTAGTATATTGACAATTTCAATGTCAAAACGAGATAAATGTGCGATTTT	300				


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Db 3592 gaaccagcaggcaatttccctcccaaggaaatgcaaccagcagcaacatcatgaagcc 3651
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Db 3652 ccggaacaacaccccccaagcaacttagaaatgcaactcagcagagctgcagggccagca 3711
OY 3631 GTTTTGAATCAGAGCCGACAGCATTGAATTGAAATGAAACCTTACTGCTGTGG 3690
Db 3712 gtcttgaatcagagccgaagccttgaaatgaaatcgaaccctactgcctgtgtg 3771
OY 3691 TGCCTCGGTATGAGCCCTATGATGAGCCGACAGGCTTCTTAATGCTCAATGCT 3750
Db 3772 tgcctcggtatgagccctatgaaatgcaagcccaagcaggttctttaaagcctaaatgtc 3831
OY 3751 CGCCCAACGACAGCAGAGCTGCTAAGTCATGCTTCGACAACAGAGGCTATGAT 3810
Db 3832 cgcacaacgacagagagctgtaagtcacatcctcgacaacagaggtgtgcatgat 3891
OY 3811 GATGACGACGAG-----CAACAGACGACGACGACGACGACGACGACGACGAC 3858
Db 3892 gatgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 3951
OY 3859 GCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCA 3918
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Db 4012 tgcctcccgacagatgatgagcttgtgacagccacacatgcccacagctcccgca 4071
OY 3979 ACAGTTTCCATATCAACCAATTATGGAATGGGACACACACAGATCCAGCTTGTGG 4038
Db 4072 acagtttccatatacacaacaaatatagaaatgggacacacacagatccagcttgtgcg 4131
OY 4039 ACTGCTAGTCTCTCCCAATGATGATGCTGCTCAAGAAATGGTCCCTCCAGATCCCAT 4098
Db 4132 actgctcagctcctcccaatgcaatgctgctcaagaaatgggtccctccagaatcccat 4191
OY 4099 GATGCAACACCCGACGGCTGATCCATCTATCATGCTCTCAGAAATGAAGGCTGGCCATC 4158
Db 4192 gatgcaaacacccgacgctgcatctcatctcagctcctcagaatgaaagctgtgcacac 4251
OY 4159 AGGAATTTGGCCAGGACAGCTCTCTTTCCAGACAGATTGGCCACAGGGGATCC 4218
Db 4252 aggaatlttggccaggaaacagctccttccagcagcagcttggccacaggggaatcc 4311
OY 4219 TGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4278
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OY 4279 GAACCCCATGCCATGCTGCGATGCTTATGGCTCTGATCAGAAATACTGCTGACATCT 4338
Db 4372 gaaccccatgcccattgctgcatgcttctgcttctgctgctgctgctgctgctgctgct 4431
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Db 4432 ctgcaacaggaactcttaagaaacactgttaacaaatgacactgcaactagatgctgctg 4491
OY 4399 AAGGAATCTTGTTCAGGCTCATCTTGAAGAAAGGACAGGCTTGAAGCTTCATCAA 4458
Db 4492 aaggaatcctgttccaggtcctcaggtcctcaggtcctcaggtcctcaggtcctcaggtc 4551
OY 4459 GGGTATTTTAACTGATGCTATTTGACAGGAAT 4491
Db 4552 gggatltttaagtgtgctcattgtgagcaggaact 4584

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 17:30:22 ; Search time 99.89 seconds
(without alignments)
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Title: US-09-041-994-1
Perfect score: 4496
Sequence: 1 GCTGATGTCGACTGACAGAG.....CATTTGACGACGATTTCTAG 4496

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

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2: /cgn2_6/ptodata/2/lna/5B.COMB.seq:*
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5: /cgn2_6/ptodata/2/lna/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74.6	1.7	397	4	US-09-253-691-3
2	73.2	1.6	168	1	US-08-469-802B-4
3	73.2	1.6	168	2	US-08-267-803B-4
4	73.2	1.6	171	1	US-08-469-802B-5
5	73.2	1.6	171	2	US-08-267-803B-5
6	73.2	1.6	195	1	US-08-469-802B-2
7	73.2	1.6	195	2	US-08-267-803B-2
8	73.2	1.6	234	1	US-08-469-802B-3
9	73.2	1.6	234	2	US-08-267-803B-3
10	68.4	1.5	154	2	US-08-469-802B-6
11	68.4	1.5	154	2	US-08-267-803B-6
12	68.4	1.5	506	1	US-08-469-802B-7
13	68.4	1.5	506	2	US-08-267-803B-7
14	68.4	1.5	3366	1	US-08-469-802B-1
15	68.4	1.5	3366	2	US-08-267-803B-1
16	68.4	1.5	10660	2	US-08-267-803B-8
17	67.6	1.5	10348	3	US-08-457-273B-41
18	67.6	1.5	10348	3	US-08-556-419-13
19	67.6	1.5	10366	1	US-08-246-982A-5
20	67.6	1.5	10366	1	US-08-453-265-5
21	66.4	1.5	3376	1	US-08-320-559-29
22	66.4	1.5	3376	3	US-08-545-860D-29
23	66.4	1.5	3376	5	PCT-US94-04496-29
24	64.8	1.4	2770	4	US-09-008-697A-13
25	64	1.4	379	4	US-08-145-617-5
26	63.2	1.4	1776	2	US-08-531-927B-1
27	60.6	1.3	543	6	5273901-6

28	59.8	1.3	1884	3	US-08-753-007A-5	Sequence 5, Appl1
29	59.8	1.3	1884	4	US-09-398-496-5	Sequence 5, Appl1
30	59.6	1.3	325	2	US-08-531-927B-3	Sequence 3, Appl1
31	59.4	1.3	4835	1	US-08-386-495-9	Sequence 9, Appl1
32	59.4	1.3	4835	5	PCT-US96-02331-9	Sequence 9, Appl1
33	58.8	1.3	533	6	5482709-5	Patent No. 5482709
34	58.4	1.3	2201	4	US-09-330-970-2	Sequence 2, Appl1
35	58.4	1.3	3336	4	US-09-330-970-4	Sequence 4, Appl1
36	57.8	1.3	3254	2	US-08-965-903B-1	Sequence 1, Appl1
37	56.6	1.3	1332	2	US-08-481-814A-3	Sequence 3, Appl1
38	56.6	1.3	1489	3	US-08-836-582-1	Sequence 1, Appl1
39	56.4	1.3	3771	1	US-08-185-432-3	Sequence 3, Appl1
40	56.4	1.3	3771	1	US-08-185-432-23	Sequence 23, Appl1
41	56.4	1.3	5063	1	US-08-185-432-1	Sequence 1, Appl1
42	56.2	1.2	3819	1	US-07-686-322A-3	Sequence 3, Appl1
43	56.2	1.2	3819	1	US-08-002-999-3	Sequence 3, Appl1
44	56.2	1.2	7498	2	US-08-816-693A-1	Sequence 1, Appl1
45	56.2	1.2	7498	3	US-08-885-291-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-09-253-691-3
; Sequence 3, Application US/09253691
; Patent No. 6124100
; GENERAL INFORMATION:
; APPLICANT: Dong Kyu JIN
; TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases
; TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
; FILE REFERENCE: 1942/36
; CURRENT APPLICATION NUMBER: US/09/253,691
; EARLIER FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: KR 98-6,278
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: WordPerfect 6.1/Windows
; SEQ ID NO 3
; LENGTH: 397
; TYPE: DNA
; ORGANISM: human
US-09-253-691-3

Query Match      1.7%; Score 74.6; DB 4; Length 397;
Best Local Similarity 71.5%; Pred. No. 1.9e-11;
Matches 98; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 3756 AACGCAGCAGACGCTGCTAGTCATCCTCCGACACAGAGGCTGCTATGATATGC 3815
Db 108 aatgtttcagcagcagcagcaaaagcagcagcagcagcagcagcagcagcagc 167

QY 3816 AGCAGCAGCAACGACGACGACGACGACGACGACGACGACGACGACGACGACG 3875
Db 168 agcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 227

QY 3876 AACGACGACAAACCCAG 3892
Db 228 agcagcagcagcagcagcag 244

RESULT 2
US-08-469-802B-4
; Sequence 4, Application US/08469802B
; Patent No. 5741645
; GENERAL INFORMATION:
; APPLICANT: Orr, Harry T.
; APPLICANT: Rannum, Laura P.W.
; APPLICANT: Chung, Ming-Yi.
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5741645
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```

: TITLE OF INVENTION: Type 1 and Method for Diagnosis
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mueeling, Raasch, Gebhardt & Schwappach, P.A.
: STREET: 119 No. 574165th Fourth Street, Suite 203
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/469, 802B
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueeling, Ann M.
: REGISTRATION NUMBER: 33,977
: REFERENCE/DOCKET NUMBER: 110,00030101
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612-305-1217
: TELEFAX: 612-305-1225
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 168 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: US-08-469-802B-4
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: Query Match 1.6%; Score 73.2; DB 1; Length 168;
: Best Local Similarity 69.7%; Pred. No. 2,8e-11;
: Matches 99; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
:
: QY 3768 AGCTGCTAAGTCATCATTCTCCGACACACAGAGGGTGGTATGATGATGCAGCAGCAGCAAC 3827
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 17 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 76
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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: QY 3888 CCACAGGCCTTCAGGCCCACTCC 3909
: ||||| ||||| |||||
: Db 137 AGCAGCAGCCTCAGCAGCGGCTCC 158
:
: RESULT 3
: US-08-267-803B-4
: Sequence 4, Application US/08267803B
: Patent No. 5834183
: GENERAL INFORMATION:
: APPLICANT: Orr, Harry T.
: APPLICANT: Rannum, Laura P.W.
: APPLICANT: Chung, Ming-yi
: APPLICANT: Zoghbi, Huda Y.
: TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
: Patent No. 5834183
: TITLE OF INVENTION: Type 1 and Method for Diagnosis
: NUMBER OF SEQUENCES: 85
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mueeling, Raasch, Gebhardt & Schwappach, P.A.
: STREET: P.O. Box 581415
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55458-1415
: COMPUTER READABLE FORM:

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REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00030101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-469-802B-5

Query Match 1.6%; Score 73.2; DB 1; Length 171;
Best Local Similarity 69.7%; Pred. No. 2.9e-11;
Matches 99; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 3768 AGCTGCTAGTCACTCTCCGACACAGAGGGTGCTATGATGCAGCAGCAGCAAC 3827
DB 20 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 79
QY 3828 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3887
DB 80 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 139
QY 3888 CCCAGGCTTCAGCCACCTCC 3909
DB 140 ACAGCAGCCTCAGCAGGGCTCC 161

RESULT 5
US-08-267-803B-5
Sequence 5, Application US/08267803B
Patent No. 5834183
GENERAL INFORMATION:
APPLICANT: Orr, Harry T.
APPLICANT: Rannum, Laura P.W.
APPLICANT: Chung, Ming-Yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-267-803B-5

Query Match 1.6%; Score 73.2; DB 2; Length 171;
Best Local Similarity 69.7%; Pred. No. 2.9e-11;
Matches 99; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 3768 AGCTGCTAGTCACTCTCCGACACAGAGGGTGCTATGATGCAGCAGCAGCAAC 3827
DB 20 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 79
QY 3828 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3887
DB 80 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 139
QY 3888 CCCAGGCTTCAGCCACCTCC 3909
DB 140 ACAGCAGCCTCAGCAGGGCTCC 161

RESULT 6
US-08-469-802B-2
Sequence 2, Application US/08469802B
Patent No. 5741645
GENERAL INFORMATION:
APPLICANT: Orr, Harry T.
APPLICANT: Rannum, Laura P.W.
APPLICANT: Chung, Ming-Yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.
STREET: 119 No. 5741645th Fourth Street, Suite 203
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muelting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00030101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-469-802B-2

Query Match 1.6%; Score 73.2; DB 1; Length 195;
Best Local Similarity 69.7%; Pred. No. 3.1e-11;
Matches 99; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 3768 AGCTGCTAGTCACTCTCCGACACAGAGGGTGCTATGATGCAGCAGCAGCAAC 3827

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RESULT      9
US-08-267-803B-3
: Sequence 3, Application US/08267803B
: Patent No. 5834183
: GENERAL INFORMATION:
: APPLICANT: Ott, Harry T.
: APPLICANT: Rannum, Laura P.W.
: APPLICANT: Chung, Ming-yi
: APPLICANT: Zoghbi, Huda Y.
: TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
: Patent No. 5741645
: TITLE OF INVENTION: Type 1 and Method for Diagnosis
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.
: STREET: 119 No. 5741645th Fourth Street, Suite 203
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/469, 802B
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Muelting, Ann M.
: REGISTRATION NUMBER: 33,977
: REFERENCE/DOCKET NUMBER: 110, 00030101
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612-305-1217
: TELEFAX: 612-305-1225
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 234 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
US-08-469-802B-3

Query Match      1.6%; Score 73.2; DB 1; Length 234;
Best Local Similarity 69.7%; Pred. No. 3.5e-11;
Matches 99; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 3768 AGCTGCTAAGTCATCACTTCCGACACAGAGGGTGGCTATGATGTCAGCAGCAGCAAC 3827
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Db 83 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 142

QY 3828 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAACGACCAACAGCAGCAAGACAGCAGCAA 3887
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Db 143 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 202

QY 3888 CCCAGGCGCTTCAGGCCCACTCC 3909
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Db 203 AGCAGCAGCCTTCAGCAGGCGCTCC 224

RESULT      9
US-08-267-803B-3
: Sequence 3, Application US/08267803B
: Patent No. 5834183
: GENERAL INFORMATION:
: APPLICANT: Ott, Harry T.
: APPLICANT: Rannum, Laura P.W.
: APPLICANT: Chung, Ming-yi
: APPLICANT: Zoghbi, Huda Y.
: TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
: Patent No. 5741645
: TITLE OF INVENTION: Type 1 and Method for Diagnosis
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.
: STREET: 119 No. 5741645th Fourth Street, Suite 203
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/469, 802B
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Muelting, Ann M.
: REGISTRATION NUMBER: 33,977
: REFERENCE/DOCKET NUMBER: 110, 00030101
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612-305-1217
: TELEFAX: 612-305-1225
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 234 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
US-08-469-802B-3

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1 COUNTRY: USA
2 ZIP: 55401
3
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Floppy disk
6 COMPUTER: IBM PC compatible
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8 SOFTWARE: Patentin Release #1.0, Version #1.25
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/08/469,802B
11 FILING DATE: 06-JUN-1995
12 CLASSIFICATION: 435
13
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Mueeling, Ann M.
16 REGISTRATION NUMBER: 33,977
17 REFERENCE/DOCKET NUMBER: 110,00030101
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: 612-305-1217
20 TELEFAX: 612-305-1225
21
22 INFORMATION FOR SEQ ID NO: 6:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 154 base pairs
25 TYPE: nucleic acid
26 STRANDEDNESS: single
27 TOPOLOGY: linear
28 MOLECULE TYPE: DNA
29
30 US-08-469-802B-6
31
32 Query Match 1.5% Score 68.4 DB 1 Length 154;
33 Best Local Similarity 71.4% Pred NO.6,1e-10;
34 Matches 90; Conservative 0; Mismatches 36; Indels 0; Gaps 0
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38 Db 2 GAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 61
39
40 QY 3827 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 3886
41 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
42 Db 62 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 121
43
44 QY 3887 ACCCAG 3892
45 |||
46 Db 122 CAGCAG 127
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48 RESULT 11
49 US-08-267-803B-6
50 Sequence 6, Application US/08267803B
51 Patent No. 5834183
52
53 GENERAL INFORMATION:
54 APPLICANT: Orr, Harry T.
55 APPLICANT: Rannum, Laura P.W.
56 APPLICANT: Chung, Ming-yi
57 APPLICANT: Zoghbi, Huda Y.
58
59 TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
60 Patent No. 5834183
61
62 TITLE OF INVENTION: Type 1 and Method for Diagnosis
63 NUMBER OF SEQUENCES: 85
64 CORRESPONDENCE ADDRESSES:
65 ADDRESSEE: Mueeling, Raasch, Gebhardt & Schwappach, P.A.
66 STREET: P.O. Box 581415
67 CITY: Minneapolis
68 STATE: MN
69 COUNTRY: USA
70 ZIP: 55458-1415
71
72 COMPUTER READABLE FORM:
73 MEDIUM TYPE: Floppy disk
74 COMPUTER: IBM PC compatible
75 OPERATING SYSTEM: PC-DOS/MS-DOS
76 SOFTWARE: Patentin Release #1.0, Version #1.25
77 CURRENT APPLICATION DATA:
78 APPLICATION NUMBER: US/08/267,803B
79 FILING DATE: 28-JUN-1994

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-267-803B-6

Query Match      1.5%; Score 68.4; DB 2: Length 154;
Best Local Similarity 71.4%; Pred. No. 6.1e-10;
Matches 90; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 3767 GAGCTGCTAAGTCATCACTTCGACACAGAGGCTGCTATGATGTCAGCAGCAGCAA 3826
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DB 62 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 121

QY 3887 ACCCAG 3892
      |||||
DB 122 CAGCAG 127

RESULT 12
US-08-469-802B-7
Sequence 7, Application US/08469802B
Patent No. 5741645
GENERAL INFORMATION:
APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESS: Mueller, Raasch, Gebhardt & Schwappach, P.A.
STREET: 119 No. 5741645th Fourth Street, Suite 203
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00030101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

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LENGTH: 506 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-469-802B-7

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Best Local Similarity 66.0%; Pred. No. 1.2e-09;
Matches 99; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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QY 3820 GCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 3879
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DB 165 GCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 224

QY 3880 GCAGCAAAACCAGCGCTTCAGCCCACTCC 3909
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DB 225 GCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 254

RESULT 13
US-08-267-803B-7
Sequence 7, Application US/08267803B
Patent No. 5834183
GENERAL INFORMATION:
APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESS: Mueller, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 506 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-267-803B-7

Query Match      1.5%; Score 68.4; DB 2: Length 506;
Best Local Similarity 66.0%; Pred. No. 1.2e-09;

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2001, 17:49:17 ; Search time 147.55 Seconds
(without alignments)
8690.439 Million cell updates/sec

Title: US-09-041-994-1
Perfect score: 4496

Sequence: 1 GCTGAGTGTGAGTACTAGAG.....CATTTGAGCAGATTTCTAG. 4496

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 195820 seqs, 142601680 residues

Total number of hits satisfying chosen parameters: 391640

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4434.2	98.6	4789	US-09-196-296B-1	Sequence 1, Appl
2	145	3.2	3361	US-09-196-296B-3	Sequence 3, Appl
3	68.4	1.5	521	US-09-815-343-422	Sequence 422, Ap
4	62.8	1.4	588	US-09-801-833-5367	Sequence 5367, Ap
5	60.6	1.3	1091282	US-09-335-032-12218	Sequence 12218, A
6	57.8	1.3	407	US-09-724-866A-24873	Sequence 24873, A
7	57.6	1.3	924430	US-09-335-032-12216	Sequence 12216, A
8	53.8	1.2	619	US-09-724-866A-12926	Sequence 12926, A
9	53.6	1.2	2685	PCT-US01-08117-154	Sequence 154, Ap
10	53.2	1.2	45333	US-60-248-505-604	Sequence 604, App
11	53	1.2	161	US-09-724-866A-8024	Sequence 8024, Ap
12	53	1.2	924430	US-09-335-032-12216	Sequence 12216, A
13	52.4	1.2	237	US-08-276-163D-12927	Sequence 12927, A
14	52	1.2	574860	US-09-335-032-12208	Sequence 12208, A
15	51.8	1.2	666448	US-09-335-032-12214	Sequence 12214, A
16	51.6	1.1	5630	US-09-709-126-1	Sequence 1, Appl
17	51.6	1.1	439885	US-09-335-032-12212	Sequence 12212, A
18	51.4	1.1	784328	US-09-335-032-12217	Sequence 12217, A
19	51.2	1.1	287	US-09-724-866A-9061	Sequence 9061, Ap
20	51.2	1.1	340	US-09-724-866A-10002	Sequence 10002, A
21	50.2	1.1	562638	US-09-335-032-12211	Sequence 12211, A
22	50	1.1	948061	US-09-335-032-12219	Sequence 12219, A
23	50	1.1	1531974	US-09-335-032-12207	Sequence 12207, A
24	49.4	1.1	3629	US-09-357-273A-1	Sequence 1, Appl
25	48.8	1.1	3046	US-09-783-514-1823	Sequence 1823, Ap
26	48.8	1.1	3046	US-09-783-514-1823	Sequence 1915, Ap
27	48.8	1.1	813137	US-09-335-032-12205	Sequence 12205, A

28	48.6	1.1	293	US-09-724-866A-15386	Sequence 15386, A
29	48.6	1.1	324	US-09-724-866A-19400	Sequence 19400, A
30	48.2	1.1	1091282	US-09-335-032-12218	Sequence 12218, A
31	47.6	1.1	391	US-09-487-566A-5303	Sequence 5303, Ap
32	47.2	1.0	183	US-09-724-866A-12068	Sequence 12068, A
33	46.6	1.0	270148	US-09-335-032-12209	Sequence 12209, A
34	46.4	1.0	471	US-09-801-833-1504	Sequence 1504, Ap
35	46.2	1.0	402	US-09-724-866A-4428	Sequence 4428, Ap
36	46.2	1.0	948061	US-09-335-032-12219	Sequence 12219, A
37	46	1.0	813137	US-09-335-032-12205	Sequence 12205, A
38	45.8	1.0	229	US-09-540-212A-32189	Sequence 32189, A
39	45.8	1.0	315341	US-09-335-032-12206	Sequence 12206, A
40	45.4	1.0	313	US-08-276-163D-4358	Sequence 4358, Ap
41	45.4	1.0	3132	US-09-533-077-320	Sequence 320, App
42	45.4	1.0	3132	US-09-739-449-3547	Sequence 3547, Ap
43	45.2	1.0	378	US-09-775-861A-54	Sequence 54, Appl
44	45.2	1.0	448	US-09-739-449-188	Sequence 188, App
45	45.2	1.0	9152	US-09-739-449-188	Sequence 188, App

ALIGNMENTS

RESULT	1	US-09-196-296B-1
Sequence 1, Application US/09196296B		
GENERAL INFORMATION:		
APPLICANT: Suen, Chen-Shian		
APPLICANT: Freil, Donald E.		
APPLICANT: Lytle, Richard C.		
TITLE OF INVENTION: Cloning and Expression of a Nuclear		
FILE REFERENCE: 0630/01376		
CURRENT APPLICATION NUMBER: US/09/196, 296B		
NUMBER OF SEQ ID NOS: 3		
SOFTWARE: FastSeq for Windows Version 3.0		
SEQ ID NO 1		
LENGTH: 4789		
TYPE: DNA		
ORGANISM: Homo Sapien		
US-09-196-296B-1		
Query Match	98.6%;	Score 4434.2; DB 5; Length 4789;
Best Local Similarity	99.3%;	Pred. No. 0;
Matches 4483; Conservative	0;	Mismatches 8; Indels 24; Gaps 2;
QY	1	GCTGAGTGTGAGTACTAGAGTAAATTAATGCTGTAACATTCCTTGACGCTT
DB	100	gctgagtggtgagctcagagaccataaataaactgttgacatcccttgactggtt
QY	61	AGCCATTGCTGATGATATTAATTAAGATGAGTGTAGAGAAATTCGATCGC
DB	160	agccattgctggtggtatattcaagatggtgattagagaaacttgatccctg
QY	121	CAGTATTCAGAAAGCAATTCGATGATGATCTCAAGCAAGCTTACTCGCAG
DB	220	cagtatttcagaaagcaaatcgcattgattccaggaagcttccctgacg
QY	181	TGTTGTAAGAAAGCAAGGAGGAGCAAGTAATTAATGAGATTTGGCTAGCTGAT
DB	280	tggtgtaaaacgagacgagcaggaagcaagaaatataatgaaatgagctgag
QY	241	ATTCGCAATCTAGAGATTAATGATTAATTCATTAATGCAAGCAATTCGATTTT
DB	340	atctgcgaatcttagagatattgcaatttcaacacgagaaatgctgagttt
QY	301	AAAGCAAGTACAGACATGCTCAATTAAGCAAGCAAGCAAGCAATTCATTCATGA
DB	400	aaagcaagtaagacagatagctcaataaagcaagcaagcaagcaatattccatga
QY	361	TGATGATGTTCAAAAGGCGCATGCTTCTACAGGCGAGGAGCTTATGATTAACATC
DB	420	tgatgatgttcaaaaggcgcatgcttctacaggcgagagcttattgataaagc


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1      CURRENT FILING DATE: 1994-07-15
2      NUMBER OF SEQ ID NOS: 15314
3      SOFTWARE: PatentIn Ver. 2.0
4      SEQ ID NO 12927
5      LENGTH: 237
6      TYPE: DNA
7      ORGANISM: Homo sapiens
8      FEATURE:
9      NAME/KEY: misc feature
10     LOCATION: (135)
11     OTHER INFORMATION: n equals a,t,g, or c
12     NAME/KEY: misc feature
13     LOCATION: (142)
14     OTHER INFORMATION: n equals a,t,g, or c
15     NAME/KEY: misc feature
16     LOCATION: (168)
17     OTHER INFORMATION: n equals a,t,g, or c
18     NAME/KEY: misc feature
19     LOCATION: (179)
20     OTHER INFORMATION: n equals a,t,g, or c
21     NAME/KEY: misc feature
22     LOCATION: (180)
23     OTHER INFORMATION: n equals a,t,g, or c
24     NAME/KEY: misc feature
25     LOCATION: (215)
26     OTHER INFORMATION: n equals a,t,g, or c
27
28 US-08-276-163D-12927

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Query Match	1.2%;	Score 52.4;	DB 4;	length 237;
Best Local Similarity	66.1%;	Pred. No. 0.00041;		
Matches 74;	Conservative	0;	Mismatches 38;	Indels 0;
			Gaps	0;

QY 3852 AGCAACAGCAACAGCAACAGCAACAGCAAAAGGCTTCAAGCCC 3903
 ||| ||| | ||||| || | | | |
 Db 106 agcagcagcagcaacacagcccggcagngccgmgagccgtcccaacc 157

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RESULT 14
US-09-335-032-12208/c
: Sequence 12208, Application US/09335032
: GENERAL INFORMATION:
:
: APPLICANT: Velculescu, Victor
: APPLICANT: Vogelstein, Bert
: APPLICANT: Kinzler, Kenneth
: TITLE OF INVENTION: Characterization of t
: TITLE OF INVENTION: Transcriptionome
: FILE REFERENCE: 01107,78572
: CURRENT APPLICATION NUMBER: US/09/335,032
: CURRENT FILING DATE: 1995-06-16
: PRIOR APPLICATION NUMBER: US 60/035,917
: PRIOR FILING DATE: 1997-01-23
: PRIOR APPLICATION NUMBER: US 09/012,031
: PRIOR FILING DATE: 1998-01-22
: NUMBER OF SEQ ID NOS: 12219
: SOFTWARE: FASTSQ for Windows Version 4.0
: SEQ ID NO 12208
: LENGTH: 574860
: TYPE: DNA
: ORGANISM: Saccharomyces cerevisiae
US-09-335-032-12208

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Query Match	1.2%	Score 52;	DB 5;	Length 574860;
Best Local Similarity	70.0%	Pred. No. 0.0043;		
Matches 70;	Conservative 0;	Mismatches 30;	Indels 0;	Gaps 0;

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15
US-09-335-032-12214/c
: Sequence 12214, Application US/09335032
: GENERAL INFORMATION:
: APPLICANT: Velculescu, Victor
: APPLICANT: Vogelstein, Bert
: APPLICANT: Kindler, Kenneth
: TITLE OF INVENTION: Characterization of t
: TITLE OF INVENTION: Transcription
: FILE REFERENCE: 01107,78572
: CURRENT APPLICATION NUMBER: US/09/335,032
: CURRENT FILING DATE: 1999-06-16
: PRIOR APPLICATION NUMBER: US 60/035,917
: PRIOR FILING DATE: 1997-01-23
: PRIOR APPLICATION NUMBER: US 09/012,031
: PRIOR FILING DATE: 1998-01-22
: NUMBER OF SEQ ID NOS: 12219
: SOFTWARE: FASTSEQ for Windows Version 4.0.
: SEQ ID NO 12214
: LENGTH: 666448
: TYPE: DNA.
: ORGANISM: Saccharomyces cerevisiae
US-09-335-032-12214

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Query Match	1.2%;	Score 51.8;	DB 5;	Length 666448;
Best Local Similarity	66.7%;	Pred. No. 0.0051;		
Matches	74;	Conservative	0;	Mismatches 37;
			Indels	0;
			Gaps	0;

Qy 3841 GCAGCAGCAGCAGCAACAGCAACAGCAGCAACAGCAACCA 3891
 ||||| ||||| || ||||| ||||| |||||
 Db 380585 ACAGCAGCAGCTACACAGCAACACAGTTGCACACACACACACACTTCA 380535

Search completed: April 29, 2001, 21:12:00
Job time: 12163 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2001, 16:45:52 ; Search time 32.49 Seconds
(without alignments)
836.669 Million cell updates/sec

Title: US-09-041-994-2
Predict score: 7.83
Sequence: 1 MSGIGENLDPLASDSRRKRL.....MNNPMMSGMPMGDPDKYC 1415

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTOS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	4.2	855	2	US-08-816-693A-2
2	307	4.2	855	3	US-08-885-291-2
3	286.5	3.9	846	3	US-08-885-291-55
4	286.5	3.9	846	3	US-09-107-847-2
5	276.5	3.7	2703	1	US-08-185-432-19
6	259	3.5	2414	1	US-08-227-536-2
7	259	3.5	2414	5	PCT-US95-04682-2
8	258	3.5	826	1	US-08-785-241-6
9	258	3.5	826	2	US-08-480-473B-2
10	258	3.5	826	2	US-08-915-213-2
11	258	3.5	826	4	US-09-148-547-2
12	258	3.5	826	4	PCT-US96-10251-2
13	254.5	3.4	816	2	US-08-785-310A-8
14	254.5	3.4	816	2	US-08-816-693A-53
15	254.5	3.4	816	3	US-08-885-291-53
16	254.5	3.4	2441	1	US-08-194-468-2
17	254.5	3.4	2441	1	US-08-961-739-2
18	252	3.4	848	1	US-08-045-806-4
19	252	3.4	848	1	US-08-366-051B-4
20	249	3.4	805	2	US-08-480-473B-4
21	249	3.4	805	3	US-08-915-213-4
22	249	3.4	805	5	PCT-US96-10251-4
23	239	3.2	810	1	US-08-785-241-7
24	237.5	3.2	870	1	US-08-785-241-4
25	233.5	3.2	824	3	US-08-885-291-52
26	230.5	3.1	824	2	US-08-816-693A-52
27	226.5	3.1	824	2	US-08-785-310A-7

28	222.5	3.0	1142	2	US-08-993-118-7	Sequence 7, Appl
29	222.5	3.0	1142	3	US-08-845-528C-7	Sequence 7, Appl
30	221	3.0	1618	1	US-07-853-913-4	Sequence 4, Appl
31	217.5	2.9	875	1	US-08-785-241-5	Sequence 5, Appl
32	217	2.9	1663	5	PCT-US93-07261-16	Sequence 16, Appl
33	212.5	2.9	3969	4	US-08-061-376-5	Sequence 5, Appl
34	204.5	2.8	805	1	US-08-045-806-2	Sequence 2, Appl
35	204.5	2.8	805	1	US-08-366-051B-2	Sequence 2, Appl
36	203.5	2.8	788	2	US-08-918-914-4	Sequence 4, Appl
37	202.5	2.7	1093	3	US-08-545-860D-55	Sequence 5, Appl
38	202.5	2.7	1093	5	PCT-US94-04496-55	Sequence 55, Appl
39	202	2.7	2842	1	US-07-741-940-7	Sequence 7, Appl
40	202	2.7	2842	1	US-08-289-548A-7	Sequence 7, Appl
41	202	2.7	2842	1	US-08-452-654-7	Sequence 7, Appl
42	202	2.7	2843	1	US-07-741-940-2	Sequence 2, Appl
43	202	2.7	2843	1	US-08-289-548A-2	Sequence 2, Appl
44	202	2.7	2843	1	US-08-452-654-2	Sequence 2, Appl
45	202	2.7	2843	1	US-08-452-655B-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-08-816-693A-2
; Sequence 2, Application US/08816693A
; Patent No. 5874241
;
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S
; APPLICANT: Turek, Fred W
; APPLICANT: Pinto, Lawrence H
; TITLE OF INVENTION: Clock Gene and Gene Product
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,693A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5874241thrup, Thomas E
; REGISTRATION NUMBER: 33,268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ. ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 855 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-816-693A-2

Query Match 4.2%; Score 307; DB 2; Length 855;
Best local Similarity 19.9%; Pred. No. 2,4e-14;
Matches 220; Conservative 149; Mismatches 373; Indels 364; Gaps 48;

QY 34 EKRRROESKYIEELAEILSANISDIDNENYKDKCAILKEIVYRIQRIKDGKTSND 93
DB 43 EKRRROFANVLKELCSMIPGNAR-----KKDKSTVLKSIIDFLRKHKR--TTAOSDA 93
QY 94 DVGKAVSVTGGQGVIDKSLGPIILQALDGFLEFVVRANIVSVSNVQYLYQKQEDLV 153
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Db 94 SEIRQDMKPT---FLSNBEFTQLMLEALDGFLLMTDGSITIIYSESVTSLEHLPSDLV 150
QY 154 NTSVYNIILHEEDRKDFELNLPKSTVNGVSWTNEPOROKSH--TFNCMYLMKPT--PHD----- 206
Db 151 DOSTFNFPBEGHSHVYKILSTHLESLSLTPREYLSKSNQLEFCCHMLRGITIDPREPSTY 210
QY 207 -----ILEDINASPE-----MRORYETWQCFR---ISQPRAMMEEGEDL 242
Db 211 EYVRFICNFKSLTYSVSTHNGFEETIQTRHPSYEDHVCFAVATRLATPOFIKE----- 265
QY 243 QSCMICVARRITTGERTPPSPNESTIRHDLGKVVNIDTMS-----LRSSMRP 291
Db 266 ---MC-----TVEEPNEFTSRHSLEMKFLFLDHRAPPIIGYLPREVIGTS--- 308
QY 292 GFEDIIRRCIORFESLNDGQSMQKRHYQEAUYLNGHAETPVYRFSLAGTIVTAQTKSKL 351
Db 309 GYD-----YHVDDLENLAKCHEHLMQY--CKGKSCYYRFLTKQOMIWIQT----- 353
QY 352 FRNPVTNDRHGCVSTHFLQREONGYRPNPNPYGQGIIRPMAGCNSSVGMSPNOGLQW 411
Db 354 -----HYIITVH-----QWNS-----RPEFIVCTHTTVVSYA-----EVRA 383
QY 412 PSSRAYGLAD--PSTYTGQMSGARVCGSS--NIASL-----TPRGQMSPSYQNN 457
Db 384 ERRRLGIEESLPETADKS--QDSGSDNRINTVYSLKALELRFHSPSPASRSRSRSS 441
QY 458 NYGLNMSPPHSGPLANOONIMISPRNRGSPKIASHQFSPVAGVHSPMSSGNTGKNS 517
Db 442 HTAV---SDPSTPYKTIPTDS--TPPRQ-----HLPAHEKMTQRRSS 479
QY 518 FSSSLSLALQAISECVGTSLSTLSSPGPKLDNSPNMNITOPSKVSNDSKSPLEGYCDQ 577
Db 480 FSSOSIN-----SQSVGSLTQ-----PAMSOANLPI--POGMSQOFQAGQ----- 521
QY 578 NPVSSMCQNSRDLHSKESKESSEVEGAENORGPLESKGKHKLIQTLTCSDDRGHSSL 637
Db 522 -----AMQHLKQLEQRTIMEANIHROQELRKIOEQLQW----- 557
QY 638 TNSPLDSSCKESSVSVTSPSGVSSSTSGVSSSTSMHGSLLQEKHRIHLKLLONGNSPAE 697
Db 558 -----VHGQGLQ-----MFLQOSN----- 571
QY 698 VAKITAQATGKDTSSI--TSCDGNVYKQEOQLSPKKKENALLRYLDDDDPSDALSKELQ 756
Db 572 -----PGLNFGSVQJSSGNSNI--QQLTP-----VNMQ 597
QY 757 POVEGVDNKMGQCTSTTIPSSQOEKDPKIKTETSESGGDLNDLAILGDLTSSDFYNN 816
Db 598 GQV-----VPANQVQ-----SGHI----- 611
QY 817 ISSNSHLGTYQOQVFOGTNSLGKSSQVOSIRPPYNRAVSLDSPVSGSSPPVKNISAF 876
Db 612 --STGOHNI-100QTLQSTIS--TQSSQSVMSGHSQOTSLPQSTPLTFLVYN----- 659
QY 877 PMLPQOPMLGCPKRMMDQOENGSSMGCPKRNKRVITYTOTPSSSDMGLPMSKAGRMMPMNSN 936
Db 660 TMVLSQPAAG-----SMVOJPSM--PQNSTQSAVTYTTFTODRQIRRSQG--QQLVTK 708
QY 937 SMGRPGGDTNLSLPPALAGSI---PILPLRSNISIPGARVLOQOQOQMLQMRPEIIMG 992
Db 709 LVTPAPVACGAVVNPSTMLMGQVYVATPTFATQOQOQO--TLSTVTOOQOQOQOQPPQOQOQ 767
QY 993 MGAN-----PYGQAASQNLGSMWPDGMLSMEOVSHGTGNRPLLRNS--LDDLVPSPNL 1044
Db 768 QOSSQEQQLPQVQOPAQAOLOQOPQOQFLOTSTRHLHGNSPTQJLILSAAVPLQOSTPSPSHH 827
QY 1045 EGQSDERALLDQJLHRLTSLNTDATGLE 1070
Db 828 QOHOPQOQOQQLPRHRTDSLTPSKVQ 853

US-08-885-291-2
; Sequence 2, Application US/08885291A
; Patent No. 6057125
; GENERAL INFORMATION:
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Turek, Fred W.
; APPLICANT: Pinto, Lawrence H.
; TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
; FILE REFERENCE: 0290-5
; CURRENT APPLICATION NUMBER: US/08/885,291A
; CURRENT FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 08/816,693
; EARLIER FILING DATE: 1997-03-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRF
; ORGANISM: Mus musculus
US-08-885-291-2

Query Match 4.2%; Score 307; DB 3; Length 855;
Best Local Similarity 19.9%; Pred. No. 2.4e-14;
Matches 220; Conservative 149; Mismatches 373; Indels 364; Gaps 48;

QY 34 EKRREQSKYIEELAEELISANLSDIDNFNVKPPKALIKETVQIROIKQEGKTTISND 93
Db 43 EKRREQSKYIEELAEELISANLSDIDNFNVKPPKALIKETVQIROIKQEGKTTISND 93
QY 94 DYQKADVSTGQGVADKSLRPLLOALDGFLLVYVREANIVFSENTOYLOKQOELV 153
Db 94 SEIRQDMKPT---FLSNBEFTQLMLEALDGFLLMTDGSITIIYSESVTSLEHLPSDLV 150
QY 154 NTSVYNIILHEEDRKDFELNLPKSTVNGVSWTNEPOROKSH--TFNCMYLMKPT--PHD----- 206
Db 151 DOSTFNFPBEGHSHVYKILSTHLESLSLTPREYLSKSNQLEFCCHMLRGITIDPREPSTY 210
QY 207 -----ILEDINASPE-----MRORYETWQCFR---ISQPRAMMEEGEDL 242
Db 211 EYVRFICNFKSLTYSVSTHNGFEETIQTRHPSYEDHVCFAVATRLATPOFIKE----- 265
QY 243 QSCMICVARRITTGERTPPSPNESTIRHDLGKVVNIDTMS-----LRSSMRP 291
Db 266 ---MC-----TVEEPNEFTSRHSLEMKFLFLDHRAPPIIGYLPREVIGTS--- 308
QY 292 GFEDIIRRCIORFESLNDGQSMQKRHYQEAUYLNGHAETPVYRFSLAGTIVTAQTKSKL 351
Db 309 GYD-----YHVDDLENLAKCHEHLMQY--CKGKSCYYRFLTKQOMIWIQT----- 353
QY 352 FRNPVTNDRHGCVSTHFLQREONGYRPNPNPYGQGIIRPMAGCNSSVGMSPNOGLQW 411
Db 354 -----HYIITVH-----QWNS-----RPEFIVCTHTTVVSYA-----EVRA 383
QY 412 PSSRAYGLAD--PSTYTGQMSGARVCGSS--NIASL-----TPRGQMSPSYQNN 457
Db 384 ERRRLGIEESLPETADKS--QDSGSDNRINTVYSLKALELRFHSPSPASRSRSRSS 441
QY 458 NYGLNMSPPHSGPLANOONIMISPRNRGSPKIASHQFSPVAGVHSPMSSGNTGKNS 517
Db 442 HTAV---SDPSTPYKTIPTDS--TPPRQ-----HLPAHEKMTQRRSS 479
QY 518 FSSSLSLALQAISECVGTSLSTLSSPGPKLDNSPNMNITOPSKVSNDSKSPLEGYCDQ 577
Db 480 FSSOSIN-----SQSVGSLTQ-----PAMSOANLPI--POGMSQOFQAGQ----- 521
QY 578 NPVSSMCQNSRDLHSKESKESSEVEGAENORGPLESKGKHKLIQTLTCSDDRGHSSL 637
Db 522 -----AMQHLKQLEQRTIMEANIHROQELRKIOEQLQW----- 557
QY 638 TNSPLDSSCKESSVSVTSPSGVSSSTSGVSSSTSMHGSLLQEKHRIHLKLLONGNSPAE 697
Db 558 -----VHGQGLQ-----MFLQOSN----- 571

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Oy 698 VAKITAAATGADKDTSSI--TSGCGDGVVYKQEDLPKSKKENNALLRYLLDRDPDSDALSKELQ 756
Db 572 -----PGINFGSVLLSSGNSNII--QQLTP-----VNNQ 597
Oy 757 PVEGEVDNKKMSQCTSSYIPSSSEOKDPKIKTERSEEGCDLIDLAILGLDITSDPFYNN 816
Db 598 GQV-----VPANQV-----SGHI-----611
Oy 817 ISSNGSLGTQKQVFGCTNSLGLKSSQSVOSIRPPYNAVLSDSPVSGSPPVKNISAF 876
Db 612 --STGQHM-100QTLQSTSS-----TOOSQSVAGSHSQSTSLPSSQTPSLTAPLTV--- 659
Oy 877 PMLCKPMPLGSPRPMMDSQENYSSNMGGPRANRTVYQTFSSGDMGLPNKAKRMEPMNSN 936
Db 660 TMTVLSQPAAG-----SMVOIPBSM-PQNSTQSATVVTFTDQRLRFSGQ--QQLYTK 708
Oy 937 SMGRPGGDYNTSLPRPALGSI-----PTLPLRNSNIPGAPRYLQOQOQMLQMKRPEIPMG 992
Db 709 LVTAPVACGAMVWPSTMLMQVYVATFTATQOQQAQ--FLSYVQOQOQOQOQPPQOQOQ 767
Oy 993 MGAN-----PYGQAASNQGLSMPDGLMSMEQVSHGTQNPFLIRNS---LDDLVEGSPNL 1044
Db 768 QOSSOEOLLEPVSQPPAQAOLGQPPQOFLQTSRLHLGNPSYTOILLASAPLQOSTPSPSHH 827
Oy 1045 EGSGDERALLDQQLHTLLSNIDATGLE 1070
Db 828 QOHOPQOQOQLPRHRTJDTLDPKAYO 853

```

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RESULT      3
US-08-885-291-55
: Sequence 55, Application US/08885291A
: Patent No. 6057125
: GENERAL INFORMATION:
: APPLICANT: Takahashi, Joseph S.
: APPLICANT: Turek, Fred W.
: APPLICANT: Pinto, Lawrence H.
: TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
: FILE REFERENCE: 0290-5
: CURRENT APPLICATION NUMBER: US/08/885,291A
: CURRENT FILING DATE: 1997-06-30
: EARLIER APPLICATION NUMBER: 08/616,693
: EARLIER FILING DATE: 1997-03-13
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 55
: LENGTH: 846
: TYPE: PRT
: ORGANISM: Homo sapiens
US-08-885-291-55

```


APPLICANT: Diederich, Robert J.
 APPLICANT: Xu, Tian
 TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
 TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PENNIE & EDMONDS
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/185,432
 FILING DATE: 21-JAN-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7326-006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ. ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2703 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-185-432-19

Query Match 3.7%; Score 276.5; DB 1; Length 2703;
 Best Local Similarity 19.1%; Pred. No. 3e-11;
 Matches 208; Conservative 147; Mismatches 383; Indels 353; Gaps 45;
 QY 455 QNNNYGLMSPRHSGGL--APRQNIKMSPRKSGPKASHQSFVAVGSHVMASSGN 512
 DB 1801 RNLNKOYAMQSGVGGAGHMSDESDMLPKQRS-----DVSQV-----GLGN 1846
 QY 513 TGNHSESSSLALQAISEGVTSL-----LSTLSPGPKLDNSPMNITOPSKVSNOD 566
 DB 1847 NGCYASHTVSEYEADQVMSAHLDVYRAIMTPRAHQDQGRH-----DVD 1896
 QY 567 SKSPGLGYCDQNPVSSCMQSNRDLSDKESKSS-----VEGAENQRPLESKG 617
 DB 1897 ARGP---CGITPLMTAAVAGGGLDGEDIEDNEDSTAYQISDLAQAEE----- 1942
 QY 618 HKLLDLTLSSSDRGHS-----LTNSPLDSSCKESVSYSPTSGVSS 662
 DB 1943 -----LNATMKTGTSTSLHARFARADAKRLFHAGADANCQDMTGRTPPLAAVAAD 1995
 QY 663 TSGGVSTSMHGSILQEKRIHLKLLQNGNSPAEVAK-----TTAQA--TGKD 709
 DB 1996 AMG-----VQOLLNRRNTNLNARHMDGTPPLILARLAIEGWEDLITADADINAAD 2048
 QY 710 TSSITSGCDGNVVKQEDLSFKKENNALRLYLDRDDPSDALSKELQPOVEGYDNKMSQC 769
 DB 2049 NSGKTALHMAAANVTBAV-----NILLMHANRD----- 2078
 QY 770 TSSITPSSQEKDPKITETSEBSGD-----LDNLDAIILGDLTSSDFYNN 815
 DB 2079 -----AODKDETPLEFLAREGSEYACKALLDNFANREITDHMDRLPRDVASERLHH 2131
 QY 816 SISNSGSHLTGKOQVFGCTSLGKSSQSVQSIIRPYNRAVSLDSPVSGSSPPVKRISA 875

DB 2132 IYRLDHEVHPSPOM-----LSMTPOAMIGSPPGQO--- 2163
 QY 876 FPMIPKOPML-----GPNPMMSQENYSSMGSPNRNVTYTQPS-----SGDWL 922
 DB 2164 QPOLITOPVYISANGN-----NGNNSAKOSNOTAKOKAAKAKLIGSPDNL 2215
 QY 923 --FNSKGRMEPMNSNMGRRGGDYNTSLPRPALG--STPTPLRNSIRGARPLYLQQ 978
 DB 2216 DATGSLRRKASSKKTSAASKKAANLGNLQTLGTVSGVGPVPPTNSAVQAAAAAAV 2275
 QY 979 QOML-QMRPEIPMGGAN--PYGQAAASNOLGSPDGMISMEQVSHGTQNPPLNLSL 1034
 DB 2276 AAMSHELEGGSPVYGWGNLPSPYDTSSMYSNMAAP--LANGNPRTGAKQPP--SY 2328
 QY 1035 DDLVPPSNLEGGSDERALLDQLHTLSTNDATGLETIDALGP--ELVNOQALEPK 1091
 DB 2329 EDICKNAQMSQSLG-----NGLDMLKLDYVAYSMSPFOQELLN--GQGLGN 2375
 QY 1092 QDAFO-QGEAAVMMQDQAGLYGOTYPAQGPMPMGGFHLOGSPSFMNMNMNOQNFPL 1150
 DB 2376 GNGORNGVGVLPBGICGNGLSGAGNNSRE-----QSLSPYSNQSPPHYSQSLAL 2430
 QY 1151 QGMHPRANIMRPTNTP-----KQLRMOLQORLQGOFLNQ----- 1186
 DB 2431 -SPHAYLGSPSPAKSLPSLPTPTTHIQMRHATQKQFGSNNLSLIGANGGVCVGG 2489
 QY 1187 -----SRQALEKMEPTAGCAVYRPMQPOQGLNOMVAORRELLSHHFQ 1236
 DB 2490 GGGGVGQGPQNSPVSIGIISPTGSDMI--MLAPQSSKNSAIMQITISPO-----Q 2539
 QY 1237 ORVAMMMQO 1296
 DB 2540 QO-----OQO 2588
 QY 1297 PQGFYQPNYMGQOPPARGVSSPPNAMS--SRMGPSQ--PMQHPOAASITVO--- 1349
 DB 2589 -----DSFHSQM-----NPPSIQSSMGSSPSTNMLSPSSQHNOQA-FYQYLT 2631
 QY 1350 -SSEMG-----WPSGNIARNSFSQ-----Q 1370
 DB 2632 PSSQHSQGHTPQHLVQTLDSYPTPSPSPGHWSSSSPSRNSDSEGVSPAANNLYISG 2691
 QY 1371 QFAHOGNPAVY 1381
 DB 2692 HQANKSEALY 2702
 RESULT 6
 US-08-227-536-2
 ; Sequence 2, Application US/08227536
 ; Patent No. 5658784
 ; GENERAL INFORMATION:
 ; APPLICANT: Ecken, Richard
 ; APPLICANT: Ecken, Richard
 ; APPLICANT: Livingston, David
 ; TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION
 ; TITLE OF INVENTION: FACTOR P300 AND USES OF P300
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Weingarten, Schurjin, Gagnedin & Hayes
 ; STREET: Ten Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/227,536
 ; FILING DATE: 14-APR-1994


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QY 734 NNALLRLLDRDDSPDALSKELOPOVEGVNKNMSOCTSTIPSSOEKDKIKETISEEG 793
DB 1849 -----SPTPA-----TPTPTGQQTPTTQTPQPTSPQ- 1875
QY 794 SGDLNLDLALDGLTSSDFYNNSSISNGSLTKQOVPQCT--NSLGKSSQSVQSTIRP 831
DB 1876 -----QTPPNSM-----PP 1885
QY 852 YNRAVSLDSPSVGS-----SPYKNISAFPMI.PKOP-----MLGNPRMMSOENYSS 901
DB 1886 YLPRTOAGAVSGKAAQVOTPTPTPTADPPLPGPPPTAVEMAKQIOTAEIOTROMA-- 1943
QY 902 MGSPPNNVTYQTPSSGDMGLPNSKAGRMEMNSNGRPGGDYNTSLPPALGGSIPTL 961
DB 1944 -----HVOIFQRIHQ--MPPMTF--MAPMGMN-----PPMTRG--PSG 1978
QY 962 PLRSNSIPGARVYLQOQO-----OMLOM--RGEIPMGCMANPYGOAASNOL 1007
DB 1979 HLE-----PGMGPTMOQOOPWMSQGLPQOOLQSGMFRPMMSVAHQGRLNMAP--QP 2031
QY 1008 GSWPDGMLSMEOVSHGTONPRLRLNSLDDLVPSPNLEGSDELRALLDOLHTLSNTDAR 1067
DB 2032 GL-----GQVGSIPKPGTVSQALQNLRLTRSPSSPLQOQO-----VLSTLH----- 2075
QY 1068 GLEIDRALGIPELVNOGALERKQDAFGQGEAIVMDOKAGLYGOTYPAQGP----- 1120
DB 2076 -----ANPOLL-----AATIKQAAKYANSNPPTIGQGPMPQ 2108
QY 1121 -----PMOGFHLQGSPPSFSNM-----NMOMNOGNFPLQGMHPRANIM 1160
DB 2109 GQGLQRPRTMGQGVNSNPAMNMNMQAGVQAGLPOQOQOQRPMSGMSPOQOM 2168
QY 1161 RPRNTN--PKOLNMQLOOQOGLNOSQALQELKMBNPPAGAAVAPRMQPOQGLNA 1219
DB 2169 NMNMNMPQSFQF--DILFRQOMQOQOQO-----OGAGPCTGPMNHNQFOQPOQGYR 2220
QY 1220 QMVAORSRELLSHHFRQORVAMMMQOQOQO-----QOQOQOQOQOQOQOQOQO 1269
DB 2221 PQRQOR-----MOHNMQOMQGNMGOIGOLPOLGAEAGSLAQOOLQOQOMSPYOPN 2276
QY 1270 AFSPR-----PNVTASPSMDGLLAGPTPQAPPOQFPYQ--PNYMGQOPDPAFQVSSPPN 1324
DB 2277 PMSPOOHMLPNOQSPHLC-----QOIPNSLSNOYRSPQVPVSPRQSPQPH 2324
QY 1325 AMMSRRGQSPQPMQHPQAASTY-----QSEBMKGWPSGMLARNSFSQOQFAHGNP 1378
DB 2325 SPSPRMQPQSPHNSPQTSPPHPLVLAQAANPMEQGFASPDQNSMLSQL-----ASNP 2380
QY 1379 AVYSVYHNMSS 1390
DB 2381 ---GMANLHGAS 2389

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RESULT 8
US-08-785-241-6
: Sequence 6, Application US/08785241
: Patent No. 5695963
: GENERAL INFORMATION:
: APPLICANT: McKnight, Steven L.
: APPLICANT: Russell, David W.
: APPLICANT: Tian, Hui
: TITLE OF INVENTION: Endothelial PAS Domain Protein
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
: STREET: 268 BUSH STREET, SUITE 3200
: CITY: SAN FRANCISCO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

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```

: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/785,241
: FILING DATE: 17-JAN-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: OSMAN, RICHARD A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: UTSD:1229
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 343-4341
: TELEFAX: (415) 343-4342
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 826 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-785-241-6

```

```

Query Match 3.5%; Score 258; DB 1; Length 826;
Best local similarity 19.8%; Pred. No. 1e-10;
Matches 181; Conservative 136; Mismatches 320; Indels 278; Gaps 41;

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QY 1 MSGIGENLD--PLASDRKRRLPCDTPGGLTSGEKKRRRQESKYIEELAILSANLSD 58
DB 1 MEGAGGANDKKKISSERKEK-----SRDAARRSRKSEVEVELAH-----QLPL 46
QY 59 IDNFNKPDKCALIKEVYR--QIRQIKGQKITSNDDVQKADVSSIGGVYIDKDSGLP 116
DB 47 PHVNSHLDKASVAVRLIYSLVRKLLDAG-DIDIEDDM-----KAQMNCPR 91
QY 117 LLOALDGLFVVRREANIVVSENVTOYLQKQEDLVNTSVNILEEDRKDFLKLNLPKS 176
DB 92 YLKALDGFVAVLIDDGDMITISDNVKNKMGLLTOPELTGHGVFPFTIRCHIEBRKMLTHR 131
QY 177 TVNG-VSMTNEPQROKS-----HTENC-----RMILKTPHDLIEDINASPEN 217
DB 152 --NGLVKKGKQONTQORSEFLRMKCTLTSGRTNIMKSAWKVLHCTGHIHYDTNSNP- 208
QY 218 RQRETMOCFALSPRAMMEGEDLDSCMTCVARRITTGERTPSNE-----SPITRH 271
DB 209 -----QCGYKKRP-----MTCVLVLEPI-----PHPSNLEIPLDSKTELSRH 246
QY 272 DLGKVVNIIDTNSLRSSMRPGF--EDIIIRCIORFESLNDQGSMSOKRHYQEAUYNLGHAE 329
DB 247 SLDMKFSYDDE--RITELMGYREBELLSIYIYHALDSHLTKTHH--DMFTKGQVY 301
QY 330 TPVYRSLADGTIVYTAQTSKLFRRNPVYNDRHGFVSTHFLQRBQNGYRPMPNPGQGI 389
DB 302 TGOYRMLAKRGYVWVETQATVIYNTKNSQPCIVCVNY----- 341
QY 390 PMACNNSVGGM-----SMSPNOGIQMPSSRAYGLADPSTTGQMSGARYCG 435
DB 342 -----VSGIIOHDLIFSLQOTECVLKVESSDMKMTOLFTRVSEDTSSFLDKLKE 333
QY 436 SSNIASLTPGPMQSPSSYONNNYGLNMS-----PPHSSPGL-APNQO-----NIM 481
DB 394 PDALITLAPAG--DITISLDFGSNDTETDQOQLEFVLYLYNDVMPSPNEKLQNTLNA 449
QY 482 ISPPNRGSPKIASHQPSPVAGVHSPMASSGNTGNHSESSSSLSALQAISEGVGTSLSTL 541
DB 450 MSP-----LPTAETPKPLRSSAD-----PALNOEVALKLT----- 478
QY 542 SSPGPKLNDSPNNINQP-----SKVSNDSKSP--LIGYQONVSSMCQ 506
DB 479 -EPNPE--SLEISFTWQLODOTPSPSDGSTQSSPEPSPSEYCYVDSDWVNEFKLE 534
QY 587 SNSRDHLSDEKSESSVEGAENQGPLESKGHKLQLLT--CSSDD-----RGHSSLTNS 640

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DB 342 -----VSGIIQDLIFSLOQTECVLKPVESSDMKMTQLETKVESEDTSSLFDKKE 393
QY 436 SSNIASLTTPGPMQSPSSYONNNYGLNMS-----PPHGSPL-APNQ-----NIM 481
DB 394 PDALTLAPAA-----DTIISLDFGSDNDETDDQLEEVPLVNDWMLSPNKKLQINILA 449
QY 442 ISPRNRGSPKIASHOFSPVAGVHSPMASSGNTGNHSSSSLSALQAISEGVSTLSLTL 541
DB 450 MSP-----LPTAETPKPLRSSAD-----PALNOEVALKL----- 478
QY 542 SSPGPKLNDSPMNTOP-----SKVSNODKSP--LGFCODNPVSSMCQ 586
DB 479 -EPNPE-----SLELFTMQIDQTPSPSDGSTKROSSPEPNSSEYCFYVDSMVNEFKLE 534
QY 587 SNSRDHLDKESKESSEVEGAENQRPLESKGHKLLQLLT--CSSD-----RGHSSLTNS 640
DB 535 LVEKLEAEDTEAK-----NPFSTQDTDLDEMLAPYIPMDDDPQLSLPQL--S 581
QY 641 PLDSS-----CKSSSVTSPPSGVSSSTSGVSTSMHGSLLQEKHRIILH-KLONG 692
DB 562 PLESSASPEASPOSTVTVFOQTQIOEPTANATTTTATDELKTVTYXDRMEDIKILIAS 641
QY 693 NSPAEVAKITAOATG---KDTSSITS---CGDG-----NVY 722
DB 642 PSPTHIHKETTATSSPYRDTOSRTASPNRACKGVIEQTEKSHPSPNVLSVALSORTTV 701
QY 723 KOEOLSPK-----KKENNAL-----RYLDRDDPSDALSKELOPOEGV--- 762
DB 702 PEEELNPKILALQNAQRKRMHDSLQAVGIGTLLQDPDHATTTLSMKRVKGCSS 761
QY 763 -DNKMSQCTSSITPS 776
DB 762 EQNGMEOKTILIPS 776

RESULT 12
PCT-US96-10251-2
Sequence 2, Application PC/TUS9610251
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10251
FILING DATE: 06-JUN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/03W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10251-2

Query Match 3.5%; Score 258; DB 5; Length 826;
Best Local Similarity 19.8%; Pred. No. 1e-10;
Matches 181; Conservative 136; Mismatches 320; Indels 278; Gaps 41;

QY 1 MSGLEND--PLASDKRRKRLPCTPGOGLTCSSEKRRREDESKYIEELAEILSANLSD 58
DB 1 MEGAGAGNDKKKISSERREK-----SRDAARSRKSESEVFEYELAH---QLPL 46
QY 59 IDNFNVKPKCAILKEAYR--OIROIKEGKTSINDDVQKADVASTGGVLDKDSLPL 116
DB 47 PHNVSSHLDKASVMKLTISYLRVKKLLDAG--DLIDEED-----KQNMCF 91
QY 117 LLQALDGELEFVNNREANIVSEANTOYLQYKQEDLVNTSVYNIILHEBRKDFLKNLPKS 176
DB 92 YLKALDGFVMVLTDDGDMITYSIDNVNKKYMGLOFELTGHSVYDDPFPNDEEMREMLNHR 151
QY 177 TVNG-VSMTNEPQOKS-----HFNCF-----RMLMTPRDILEDINAPEM 217
DB 152 --NGLVKKGKEQNTQRFELRMKCTLSRGRTMNKSAWKVLCGHIIHYDTSNQP- 208
QY 218 RQRYETMOCFALSOPTAMEBEGEDLQSCMICVARRITTGERTFSPNPE-----SFTRH 271
DB 209 -----QCGYKRP-----MTCLVLICEPT-----PHPSNIEPLDLSKTFELSRH 246
QY 272 DLSGKVNIDTNSLRSMRPF--EDIRRCIQRPFSLNDGSMQKRYOEAYLNGHAE 329
DB 247 SLDMKFYVCD--RITELMGEPPELLGRSLEYEYHALDSDHLKTHH--DMFTKGGVT 301
QY 330 TPVYRPSLADGITVTAQTKSKLEFRNPVINDRGVSTFPLEQDNGYRPNRPVQGGIRP 389
DB 302 TGQYRMLAKRGYVWVETQATVYNTKNSQPCICVNVV----- 341
QY 390 PMAGCNSSVYGM-----SMSNQGLOMPSRAYGLADPSTTGOMSGARYG 435
DB 342 -----VSGIIQDLIFSLOQTECVLKPVESSDMKMTQLETKVESEDTSSLFDKKE 393
QY 436 SSNIASLTTPGPMQSPSSYONNNYGLNMS-----PPHGSPL-APNQ-----NIM 481
DB 394 PDALTLAPAA-----DTIISLDFGSDNDETDDQLEEVPLVNDWMLSPNKKLQINILA 449
QY 442 ISPRNRGSPKIASHOFSPVAGVHSPMASSGNTGNHSSSSLSALQAISEGVSTLSLTL 541
DB 450 MSP-----LPTAETPKPLRSSAD-----PALNOEVALKL----- 478
QY 542 SSPGPKLNDSPMNTOP-----SKVSNODKSP--LGFCODNPVSSMCQ 586
DB 479 -EPNPE-----SLELFTMQIDQTPSPSDGSTKROSSPEPNSSEYCFYVDSMVNEFKLE 534
QY 587 SNSRDHLDKESKESSEVEGAENQRPLESKGHKLLQLLT--CSSD-----RGHSSLTNS 640
DB 535 LVEKLEAEDTEAK-----NPFSTQDTDLDEMLAPYIPMDDDPQLSLPQL--S 581
QY 641 PLDSS-----CKSSSVTSPPSGVSSSTSGVSTSMHGSLLQEKHRIILH-KLONG 692
DB 562 PLESSASPEASPOSTVTVFOQTQIOEPTANATTTTATDELKTVTYXDRMEDIKILIAS 641
QY 693 NSPAEVAKITAOATG---KDTSSITS---CGDG-----NVY 722
DB 642 PSPTHIHKETTATSSPYRDTOSRTASPNRACKGVIEQTEKSHPSPNVLSVALSORTTV 701
QY 723 KOEOLSPK-----KKENNAL-----RYLDRDDPSDALSKELOPOEGV--- 762
DB 702 PEEELNPKILALQNAQRKRMHDSLQAVGIGTLLQDPDHATTTLSMKRVKGCSS 761
QY 763 -DNKMSQCTSSITPS 776
DB 762 EQNGMEOKTILIPS 776

RESULT 13
US-08-785-310A-8

```

: Sequence 8, Application US/08785310A
: Patent No. 5840532
: GENERAL INFORMATION:
: APPLICANT: McKnight, Steven L.
: TITLE OF INVENTION: Neuronal PAS Domain Protein
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
: STREET: 268 BUSH STREET, SUITE 3200
: CITY: SAN FRANCISCO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/785,310A
: FILING DATE: 21-JAN-1997
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: OSMAN, RICHARD A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: UTSD:1226
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 343-4341
: TELEFAX: (415) 343-4342
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 816 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-785-310A-8

Query Match      3.4%; Score 254.5; DB 2; Length 816;
Best Local Similarity 21.1%; Pred. No. 1.8e-10;
Matches 194; Conservative 137; Mismatches 346; Indels 241; Gaps 47;

QY 34 EKRRRQESKYEIEELALLISANLSDIDFNFKPKCALIKETVQIQOIKEGQTTIND 93
DB 18 EKRRRQGFNVLKELSSMLPGNFR-----KMDRTVLKRYIGFLQKHNE---VSAQT 66
QY 94 DVOKADVSTGCG-VDIKDLSLGPLLLOALDGLFVVRNREANIVFSENMVQYLOKQEDL 152
DB 67 EI--CDIQOMKRSFSLNEFEFTQMLALDGFYIVTTDGSIIYVSDSTIPPLGHLPADV 124
QY 153 VNTSVYNIHEEDRKDELKMLPKSTVNGVSWTNEPQOKSHT--FNCRLMLKTPHDILE 209
DB 125 MDQULNLFPEQHESEYKILTSMLL--VYDPSPEFLKSDNDEFLCHLLRG----- 175
QY 210 DINASPMRORYETMOCF-----ALSOPRAMEEGEDLOSCHICVA 250
DB 176 --SLNPKPEFTYEIKKIVGNFRSYNVPSPSCNGFDMTLNRP-CHVPLGADV--CFIATV 230
QY 251 RRIIT--TGERTPSPN-ESFTRHDLGKGVNIDTNS-----LRSSMRPGEF- 294
DB 231 RLATPOLKEMCYADELLEFTSHSLKWKFLFLDHRAPPLIGLPLEVLGTS---GINY 287
QY 295 -----DIIRRCIQRFSLNDGOS-----WSQKRHYQEAY--LNGHAETPVY 333
DB 288 YHIDDELARHQHLMQFGKSKSCYRPLTKGQWIMLQ--THYITLYHQMNSKEPIYVC 346
QY 334 RPSLADGTIYTAQTKSL-FRNPVTNDRHGFSVTHPLQREONGRPNPNVPGQ---GIRP 389
DB 347 THSVYADYADYVERKDELALDEDPTEAMH-----PSAVKEDKDSLEP 388
QY 390 PMAGCNSVGMKSPMNGLOMPSSRAYGLADPSTTGMSGARGYSSNLIASLTPGGMQ 449

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DB 389 P-----QPPNALDM-----GASGLPS-SPSSSAS 411
QY 450 SPSSYONNNYGLNKSPPHSPGLAQNQIMISPRNRGSPKIASHOFSVAGVHSPMAS 509
DB 412 SRSSHKSSHTAM--SEPTSTPKLMAENSTALPRPATLP-----QELPVQCL--SQAA 461
QY 510 SGUNGNHSPSSSLSS--ALQATISEGVSTLSLTLSPGKLDNSPMMNITOPSKVSNOD 566
DB 462 TMTPLHSSASCDLTQKLLQSLPO--TGL--QSPPAVYTOPSAQFSMEOTIK----- 510
QY 567 SKSLPGFYCDQNPVSSMCSNSRDLSDKESKESVEGAENRGPLESGHKKLLQ--- 623
DB 511 -----DQLEGRTRILQANIR-----WQOEELHKIQEOLCLVQDSNQMFLQOPRA 554
QY 624 -LITCSSDDR--GHSLTNSPLDSSCKESSVYTPSPGVSSTSGVSTSNMHSGLQ 660
DB 555 VSLSFSTQRPAAQOOLQGRPAVS--QPOLVYVTP-----LQGLTSTQVQNHLLRE 606
QY 681 KHRILHLKLLONGNSPAVAKITATQATKDRSSITSCGDGVNVQEOQLSPKKENMLLRY 740
DB 607 SMTI---SAQGRPMKSSQL-LPASGRSLSLPS-----QFSSTASYLPPGLSL 651
QY 741 LLDHDDPSDALSKELQOVE-GVDNK-----MSQCTSTIPSSQEKDPKIKTETSEBGS 795
DB 652 TTIAPTPQD--DSQCGSPPGHGRQLRLLSQIOPMFGSCDARQ---SEVSRTRGQ 706
QY 796 DLNDLAIIDLTLSSDFYNSISSNSGSLGTQOY---FQGTNSLGLKSSQSVQSTIRP 851
DB 707 VKYAQSQVMFPSPSHPTNSSASAPVLLMG--QAVLHPSPAPSRPPLQAQAQOQO--PP 763
QY 852 YNRAVSLDSPVSVSSPP 869
DB 764 Y-----LQAPTSLSHSEQ 776

RESULT 14
US-08-816-693A-53
: Sequence 53, Application US/08816693A
: Patent No. 5874241
: GENERAL INFORMATION:
: APPLICANT: Takahashi, Joseph S
: APPLICANT: Turek, Fred W
: APPLICANT: Pinto, Lawrence H
: TITLE OF INVENTION: Clock Gene and Gene Product
: NUMBER OF SEQUENCES: 53
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/816,693A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5874241thrup, Thomas E
: REGISTRATION NUMBER: 33,268
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5460
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 53:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 816 amino acids
: TYPE: amino acid
: STRANDEDNESS: single

```

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-816-693A-53

Query Match 3.4%; Score 254.5; DB 2; Length 816;

Best Local Similarity 20.8%; Pred. No. 1.8e-10; Indels 231; Gaps 45;

Matches 190; Conservative 140; Mismatches 352;

34 EKRRROESKYIELELAELISANLSDIDNENVPDKCALIKETVROIRQIEQKTIISND 93
18 EKRRDQEVNLKELSSMLPGNIR-----KMDKITVLEKVIQGLQKNE---VSAQT 66
94 DVQKADVSSTGO-GVIDKDSLAPLLQALDGLFVYNREANIVFSENVTOYLQKQEDL 152
67 EI--CDIQQDMKPSFLSNEEFTQMLLEALDGFVIYVTTGSGIIYVSDSTPLGLHLPADV 124
153 VMTSVYNIHEDRKDFLNLKSTVNGSVMTNEPQROKSHT---FNCMLMKTPIHDLE 209
125 MDONLNLFPEDQHSFVYKILSSHML--VTDSPPEFLKSDNDLEFYCHLLRG----- 175
210 DINASPEMRQREYTMQCF-----ALSOPRAMEGEGEDLOSCMICVA 250
176 --SLNPKPEPTVEYIKFVGNFRSYNNVPSPCNGFDNLTSLRP-CHVPLGKDV--CFIATV 230
251 RRIIT---TGERTFPSNP-ESFTRHDLSGKYVNIIDTNS-----LRSSMRPGE- 294
231 RLATPOFLKEMCVADEPLEEFTSRHSLEWKFLDHRAPPIIGYLPFEVLGTS---GYNY 287
295 -----DIRRCIORFFSLNDGOS-----WSQKHGYEAY--LNGHAETPY 333
288 YIIDDELLARCHOHLMOFGKSCCYRFLTKGQOWIMLQ--THYITTYHOMNSKPEFTVC 346
334 RFLSLADGITVIAQTQSKL-FRNPVTNDRHGFVSTHFLQREQNGYRPNPNVQO---GIRP 389
347 THSVSYADVAVRERQELALEDPTEPAH-----PSAVKEXKSSLEP 388
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389 P-----QPFNALDM-----GASGLPS-SPSPSAS 411
450 SPSSYONNNYGLNMSPPHSGPLAPNOONIMISPRNGSPKIASHQPSPVAGVSPMAS 509
412 SSSSHKSSHTAM---SEPTSTPTKLAENSTALPRATLP-----QELPYOGL--SOAA 461
510 SCNTGNHSSFSSSLS---ALQAISEGVGTSLLSTLSSPGKLDNSPNNNITOPSKVSNOD 566
462 TMPRLALHSSASCDLTQKLLQSLPQ---TGL---QSPAPVYQFSAQSMQOTIK----- 510
567 SKSPLEGYCDQNPVSSMCOQNSRDHLSDEKESSEVGEAENQGRPLESKGHKKLLQLT 626
511 -----DOLEQRTIRLIQANIR-----WQOEELKHIQEOCLCYODSNVQMFLOQPA 554
627 CSSDDRGHSLNPLSDSCCKESSVSVTSPS-GVSSSTSGVSTSNMHSGLDEKHKIL 685
555 VS--LSPFSIORPAAQOQLQRPAPAPSPOLVNTPLQGTITQVYTHQHLRESNV- 610
686 KHLLONGNSPRAVAKITTAQATGKTJSTSCGDGVNKKOEQLSPKKKENNALLRYLLDRD 745
611 ---SAQGRPKMRSQD-LPASGRSLSLPS-----QFSSTASVLPGLSLTTIAP 656
746 DPSDALSKLQOVE-GVDNK---MSOCTSTTIPSSSEKQPKIKTEISEGSGDLML 800
657 TPQD--DSOCQSPDFGCHDRQLRLLSQPIQPMMPESCDARP---SEVSRTGROYKAYAO 711
801 DALIGDITSSDFYNNSSISSNGSHLGTQOY---FOGTNSLKLSSQSOVSTRPYNRAV 856
712 SQVMPSPDSHPTNSASAPVLLMG--QAVLHPSFPASAPSLQRAQAOQO--PPPY----- 764
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RESULT 15
US-08-885-291-53
Sequence 53, Application US/08885291A
Patent No. 6057125

GENERAL INFORMATION:
APPLICANT: Takahashi, Joseph S.

APPLICANT: Turek, Fred W.

APPLICANT: Pinto, Lawrence H.

TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT

FILE REFERENCE: 0290-5

CURRENT APPLICATION NUMBER: US/08/885,291A

CURRENT FILING DATE: 1997-06-30

EARLIER APPLICATION NUMBER: 08/816,693

EARLIER FILING DATE: 1997-03-13

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 53

LENGTH: 816

TYPE: PRT

ORGANISM: Mus musculus

US-08-885-291-53

Query Match 3.4%; Score 254.5; DB 3; Length 816;

Best Local Similarity 20.8%; Pred. No. 1.8e-10; Indels 231; Gaps 45;

Matches 190; Conservative 140; Mismatches 352;

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94 DVQKADVSSTGO-GVIDKDSLAPLLQALDGLFVYNREANIVFSENVTOYLQKQEDL 152
67 EI--CDIQQDMKPSFLSNEEFTQMLLEALDGFVIYVTTGSGIIYVSDSTPLGLHLPADV 124
153 VMTSVYNIHEDRKDFLNLKSTVNGSVMTNEPQROKSHT---FNCMLMKTPIHDLE 209
125 MDONLNLFPEDQHSFVYKILSSHML--VTDSPPEFLKSDNDLEFYCHLLRG----- 175
210 DINASPEMRQREYTMQCF-----ALSOPRAMEGEGEDLOSCMICVA 250
176 --SLNPKPEPTVEYIKFVGNFRSYNNVPSPCNGFDNLTSLRP-CHVPLGKDV--CFIATV 230
251 RRIIT---TGERTFPSNP-ESFTRHDLSGKYVNIIDTNS-----LRSSMRPGE- 294
231 RLATPOFLKEMCVADEPLEEFTSRHSLEWKFLDHRAPPIIGYLPFEVLGTS---GYNY 287
295 -----DIRRCIORFFSLNDGOS-----WSQKHGYEAY--LNGHAETPY 333
288 YIIDDELLARCHOHLMOFGKSCCYRFLTKGQOWIMLQ--THYITTYHOMNSKPEFTVC 346
334 RFLSLADGITVIAQTQSKL-FRNPVTNDRHGFVSTHFLQREQNGYRPNPNVQO---GIRP 389
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 Job time: 296 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2001, 16:45:53 ; Search time 147.68 Seconds
(without alignments)
1541.232 Million cell updates/sec

Title: US-09-041-994-2

Perfect score: 7383
Sequence: 1 MSGUGENDPLASDSRRKRL.....MNNMPMPSGMPKGPDKKXC 1415

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1009251 seqs, 160854530 residues

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	7375	99.9	1415	US-09-513-066-2	Sequence 2, Appl1
3	7352.5	99.6	1420	US-09-125-635-4	Sequence 4, Appl1
4	6077.5	82.3	1402	US-09-125-635-12	Sequence 12, Appl1
5	5864.5	79.4	1398	US-09-513-066-14	Sequence 14, Appl1
6	5411	73.3	1402	US-09-445-353A-2	Sequence 2, Appl1
7	5041	68.3	1391	US-09-513-066-15	Sequence 8, Appl1
8	4938	66.9	951	US-09-125-635-8	Sequence 15, Appl1
9	2740.5	37.1	1464	US-08-891-640-2	Sequence 2, Appl1
10	2717.5	36.8	1462	US-09-445-353A-3	Sequence 3, Appl1

11	1966.5	26.6	1127	US-60-258-273-113	Sequence 113, App
12	957	13.0	186	US-09-125-635-2	Sequence 2, Appl1
13	873	11.8	1036	US-08-891-640-3	Sequence 3, Appl1
14	872	11.8	1061	US-08-701-154A-5	Sequence 5, Appl1
15	742	10.1	149	US-60-236-359-19468	Sequence 19468, A
16	739.5	10.0	147	US-08-766-263-2	Sequence 2, Appl1
17	739.5	10.0	147	US-08-766-263A-2	Sequence 2, Appl1
18	739.5	10.0	147	US-08-989-237-2	Sequence 2, Appl1
19	739.5	10.0	147	US-09-398-828-134	Sequence 134, App
20	644	8.7	124	US-60-182-515-11	Sequence 11, Appl
21	636.5	8.6	125	US-60-177-667-98	Sequence 98, Appl
22	530.5	7.2	106	US-60-196-714-414	Sequence 414, App
23	396.5	5.4	1778	US-60-191-637-7056	Sequence 7056, App
24	396.5	5.4	1778	US-60-173-464-19825	Sequence 5523, App
25	379.5	5.1	1625	US-60-173-464-5755	Sequence 5755, App
26	376	5.1	73	US-09-125-635-3	Sequence 3, Appl1
27	351.5	4.8	3275	US-60-191-637-37720	Sequence 37720, A
28	351.5	4.8	3275	US-60-191-637-29308	Sequence 29308, A
29	347.5	4.7	4007	US-60-173-464-19825	Sequence 19825, A
30	337.5	4.6	75	US-60-196-714-529	Sequence 529, App
31	334	4.5	2976	US-60-171-627-1856	Sequence 1856, App
32	334	4.5	2976	US-60-173-464-26918	Sequence 26918, A
33	334	4.5	2977	US-60-191-637-34837	Sequence 34837, A
34	334	4.5	2977	US-60-191-637-27367	Sequence 27367, A
35	333	4.5	5222	US-60-245-201-208	Sequence 208, App
36	329.5	4.5	3059	US-60-167-217-21631	Sequence 21631, A
37	329.5	4.5	3059	US-60-171-627-1719	Sequence 1719, App
38	329.5	4.5	3059	US-60-173-464-17597	Sequence 17597, A
39	325.5	4.4	1366	US-60-191-637-27784	Sequence 27784, A
40	325.5	4.4	1366	US-60-191-637-22393	Sequence 22393, A
41	325.5	4.4	1594	US-60-191-637-17909	Sequence 17909, A
42	325.5	4.4	1594	US-60-191-681-11162	Sequence 11162, A
43	325	4.4	2280	US-09-619-049-654	Sequence 624, App
44	325	4.4	2280	US-60-167-217-11753	Sequence 11753, A
45	325	4.4	2280	US-60-171-627-975	Sequence 975, App

ALIGNMENTS

RESULT 1
US-09-041-994-2
Sequence 2, Application US/09041994
GENERAL INFORMATION:
APPLICANT: Chen, J. Don
TITLE OF INVENTION: Transcriptional Coactivator for Nuclear
TITLE OF INVENTION: Hormone Receptors
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,994
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Liepmann, W. Hugo
REGISTRATION NUMBER: 20,407
REFERENCE/DOCKET NUMBER: UMM-026-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-742-7400
TELEFAX: 617-742-4214
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
; LENGTH: 1415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-041-994-2

Query Match 100.0%; Score 7383; DB 14; Length 1415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-513-066-2
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; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; APPLICANT: Leo, Christopher
; APPLICANT: Li, Hui
; TITLE OF INVENTION: NOVEL USES FOR THE RAC3 TRANSCRIPTIONAL COACTIVATOR OF
; FILE REFERENCE: UMG-026CP
; CURRENT APPLICATION NUMBER: US/09/513, 066
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: USSN 09/041, 994
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: USSN 60/073, 674
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-066-2

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Matches 1414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1201 GGAAYWRPMQPOQGFNLNQMTAORSRELLSHHFROQRYAMMM-----0000000000 1255
Db 1201 GGAAYWRPMQPOQGFNLNQMTAORSRELLSHHFROQRYAMMM-----0000000000 1255
Qy 1255 QOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 1315
Db 1255 QOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 1315
Qy 1315 FERVSSPPRMAAMSSRKQSPQNMQHPQAASTYOSSEMKGWSGNLARNSSFOQFAHQ 1375
Db 1315 FERVSSPPRMAAMSSRKQSPQNMQHPQAASTYOSSEMKGWSGNLARNSSFOQFAHQ 1375
Qy 1375 GNPAYVSNVHMNGSSGHMGOMMNPMPMSGMPMGPOKXC 1415
Db 1375 GNPAYVSNVHMNGSSGHMGOMMNPMPMSGMPMGPOKXC 1415
Qy 1415 GNPAYVSNVHMNGSSGHMGOMMNPMPMSGMPMGPOKXC 1420
Db 1415 GNPAYVSNVHMNGSSGHMGOMMNPMPMSGMPMGPOKXC 1420

RESULT 4
US-09-125-635-12
: Sequence 12, Application us/09125635
: GENERAL INFORMATION:
: APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
: TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
: FILE REFERENCE: 49944
: CURRENT APPLICATION NUMBER: US/09/125,635
: CURRENT FILING DATE: 1998-08-21
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: PRIOR APPLICATION NUMBER: 60/049,728
: BEST FILING DATE: 1997-06-17
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: Patent Ver. 2.0
: SEQ ID NO 12
: LENGTH: 1402
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-125-635-12

Query Match      82.3% Score 6077.5 DB 15 Length 1402:
Best Local Similarity 81.7% Pred No. 0:
Matches 1175; Conservative 85; Mismatches 118; Indels 61; Gaps 11:

Qy 1 MSGLGE-NIDPLASRRKKRLPCDTPPGQGLTCSGEKRRRQESKYIEELAEILSANLSDI 59
Db 1 MSGLGESSLDPLAESRRKKRLPCDAPGQGLVYSGEKWRREQSKYIEELAEILSANLSDI 60
Qy 60 DNFNPKPKCALIKETVROIROIKEDGKTISSDDVQKADVSTGCGYIDKDSLGLPLLLQ 119
Db 61 DNFNPKPKCALIKETVROIROIKEDGKTISSDDVQKADVSTGCGYIDKDSLGLPLLLQ 120
Qy 120 ALDGLFVYNNREANITVESENTVOYLQYKQEDLVMTSVYNTLHEDRDKFLKNLPKSTYN 179
Db 121 ALDGLFVYNNRGNTIYVESENTYQYKQEDLVMTSVYSLHEDRDKFLKNLPKSTYN 180
Qy 180 GVSMTNEPQROKSHTFNCBMLKTPHILIEDINASPENRORYETMQCFALISOPRAMMEBG 239
Db 181 GVSMTNENQROKSHTFNCBMLKMT-HDILEDVNASPETRQRETQMOCFALISOPRAMMEBG 239
Qy 240 EDLQCMICVARRITTEGTPSPNPBSFTTRHDLGKVVNIDTNSLRSSMRPGFEDIIR 299
Db 240 EDLQCMICVARRITTEGTPSPNPBSFTTRHDLGKVVNIDTNSLRSSMRPGFEDIIR 296
Qy 300 CIQRFPSLNDGQSWGSKRHQOEAAYLNGHAEPTVYRPSLADGRTIWAQTKSLFRPVPND 359
Db 297 CIQRFPSLNDGQSWGSKRHQOEAAYLNGHAEPTVYRPSLADGRTIWAQTKSLFRPVPND 356
Qy 360 RHGFVSTHFLQEQNGYRPNPVPVGGIRPPMAGCNSSVSGMSMSPNOGLQMPSSRAYGL 419
Db 357 RHGFISTHFLQEQNGYRPNPVPVGGIRPPMAGC-----GVSMSPNQVQMMGSRRTGY 411
Qy 420 ADPSTTGQNSGARVGGSSNIALTPGCMQSPSTIONNNTGLNMSSPPHSGGLAPNQON 479
Db 412 PDPSTNGQNGARVSSVASTLPQOGLQSPSSYQNSSYGLSMSPPHSGGLAPNQON 471
Qy 480 IMISPRNRSPPKIASHOFSPVAGVHSPMASGNTGHNHSPSSSLAIAQISRGVCTSLIS 539
Db 472 IMISPRNRSPPKIASHOFSPAAGAHSPMGPSGNTGSHFSSSLAIAQISRGVCTSLIS 531
Qy 540 TISSPGKLDNSBNMNTOPSKVSNODSKSPGLFYCDQNFVESSMCOSSNRDLSDKESK 599
Db 532 TISSPGKLDNSBNMNTOPSKVSNODSKSPGLFYCDQNFVESSMCOSSNRDLSDKESK 591
Qy 600 ESSVEGAENQGRPLESGHKKLLQLLTCCSSDDRGHSLTNSPLDSSCKESSVYTSRSGV 659
Db 592 ESSVEGAENQGRPLESGHKKLLQLLTCCSSDDRGHSLTNSPLDSSCKESSVYTSRSGV 651
Qy 660 SSTSGVSTSMNHGSLLOEKHRIHLKLLQNGNSPAEVAKITAQATGKXTSSITSCGDG 719
Db 652 SSTSGVSTSMNHGSLLOEKHRIHLKLLQNGNSPAEVAKITAQATGKXTSSITSCGDG 711
Qy 720 NVVKOEOLSPKKENNALRYLLDRDDPSDALSKELQPOVEGVNKNMSQCTSSITPSSOE 779
Db 712 NVVKOEOLSPKKENNALRYLLDRDDPSDALSKELQPOVEGVNKNMSQCTSSITPSSOE 770
Qy 780 KKPRTKETSESGDLDNLDAIILGDLTSSDFYNNSSISNGSHLTKQOYFQGTNSLGLK 839
Db 771 KKPRTKETSESGDLDNLDAIILGDLTSSDFYNN--PTNGHGAGQOQMFAGSSLGL 828
Qy 840 SSOSVOSTRPPYNNRAVSLDSPVSVGSSPPVKNISAFPMILPKQPMILGPNRMDSOENYGC 899
Db 840 SSOSVOSTRPPYNNRAVSLDSPVSVGSSPPVKNISAFPMILPKQPMILGPNRMDSOENYGC 899
```


PRIOR APPLICATION NUMBER: USSN 09/041,994
 PRIOR FILING DATE: 1998-03-13
 PRIOR APPLICATION NUMBER: USSN 60/073,674
 PRIOR FILING DATE: 1998-02-04
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO 15
 LENGTH: 1391
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-09-513-066-15

Query Match 68.3%; Score 5041; DB 19; Length 1391;
 Best Local Similarity 69.8%; Pred. No. 0;
 Matches 998; Conservative 161; Mismatches 217; Indels 54; Gaps 24;

1 MSGIGEN-LDPLASDSRRK-LPCDTPGQGLTSCGKRRRDESKYIEELAEILSANLSD 58
 1 MSGIGENSLDPLASERKRRKPPGGLTSCGKRRRDESKYIEELAEILSANLSD 60
 59 IDNFNKKPKCALKTETVQIRQIKQGTISNDVDYQKADVSTGQGYIDKDSLGLPL 118
 61 IDNFNKKPKCALKTETVQIRQIKQGTISNDVDYQKADVSTGQGYIDKDSLGLPL 120
 119 QALDGLFVYNREAPVSEVNTQYLOKQEDLVNTSVNLIHEDRKDFLNEKSTY 178
 121 QALDGLFVYNREAPVSEVNTQYLOKQEDLVNTSVNLIHEDRKDFLNEKSTY 180
 179 NGVSTNEPQROKSHTEFNCRLMKTPHDLEINASPEMROREYEQCFALSOPTAMEE 238
 181 NGVSTNEPQROKSHTEFNCRLMKTPHDLEINASPEMROREYEQCFALSOPTAMEE 239
 239 GEDLOSCMTCVARRITTEGERTPEPSPESFTRHDSGKVVNIDTNSLRSSMRPFEDI 298
 240 GEDLOSCMTCVARRITTEGERTPEPSPESFTRHDSGKVVNIDTNSLRSSMRPFEDI 299
 299 RCTQREFSLNDGOSMSOKRHYOEAFLYVHAETPVYRFSIADGTIVTAQRTSKLFRNPVTN 358
 300 RCTQREFSLNDGOSMSOKRHYOEAFLYVHAETPVYRFSIADGTIVTAQRTSKLFRNPVTN 359
 359 DRHGFVSTHFLQREQNGYRPNPVPVQGITRPMACNSVY-GGMSMSPNOGLQMPSSRAY 417
 360 DRHGFVSTHFLQREQNGYRPNPVPVQGITRPMACNSVY-GGMSMSPNOGLQMPSSRAY 415
 418 GLADPSTQMGARYGSSNTASLTTPGQMOSSSYQNN-NYGLMSSPFGHSPGIAPN 476
 416 GMDPNSMAQMGMRKSPGNMAYVQAGVQO-SFYQNNNSYGLMNSPFGHSPGMANAN 474
 477 QONIMSPNRSRGTASHQFSPVAGVHSPMASSGNTGHNHSPSSSLSLALQASEGVTS 536
 475 QONIMSPNRSRGTASHQFSPVAGVHSPMASSGNTGHNHSPSSSLSLALQASEGVTS 534
 537 LLSLSSPGPKLDNSPNMNTTOPSKVSNODSKSPPLGFYCDQNPVSSMCOSSRDLSDK 596
 535 LLSLSSPGPKLDNSPNMNTTOPSKVSNODSKSPPLGFYCDQNPVSSMCOSSRDLSDK 594
 597 ESKSEVEGAENQGLPESGKHKLLQLLTCSDDRGHSLTNSPLDSSCKESSVSTSP 656
 595 ESKSEVEGAENQGLPESGKHKLLQLLTCSDDRGHSLTNSPLDSSCKESSVSTSP 651
 657 SGVSSSTSGVSTSMHMSLLOEKHRIILKLLQNGNSPRAEVAKITQAOTGKDP-----TSS 712
 652 SGVSSSTSGVSTSMHMSLLOEKHRIILKLLQNGNSPRAEVAKITQAOTGKDP-----TSS 711
 713 ITSCGDNVAVKQOLSPKKKENNALLRYLLDRDPDSDALSKELQPOVEGADNKSCTSS 772
 712 ITSCGDNVAVKQOLSPKKKENNALLRYLLDRDPDSDALSKELQPOVEGADNKSCTSS 770
 773 TTPSSQEKDPTKITETSEBGSDLDNLDAIIGDLTSSDFYNNISISSNGSLGCKQVFO 832
 771 TTPSSQEKDPTKITETSEBGSDLDNLDAIIGDLTSSDFYNNISISSNGSLGCKQVFO 830

833 GTNSLGLKSSQSVOSIRPPYNNRAVSLDSPVSGSPPVKNISAFMLPKOPMLGNPRM 892
 831 DSFTLAMRSPDSMQSRPPENRAMSLDSR---STTPYRVNVSFPLPKQGM-GSPRMM 886
 893 DSGENTGSSMG-GPNRVYVYTOTPSSGDMGLPNSKAGRMENPNSNGRPGDYNTSLR 951
 887 DGDNFGVMWGSQPNR-SMNQHP-GGDMAQNSAVNRLEPPVSGVGRGPDYSAMTR 943
 952 PALGSIPTPLPLANSITPGARVYLQOQOOLQMRPEIIRPKGANKANYGOAASNOGLSP 1011
 944 PALGSIPTPLPLANSITPGARVYLQOQOOLQMRPEIIRPKGANKANYGOAASNOGLSP 1003
 1012 DGLMSMEVYSHGTQNPRLRNSLDDLVGPSPNSEGSDERALLDOLHTLLSNTDAGLE 1071
 1004 DAIM-MNQRGCAQNLQGRNSLDDLVGPSPNSEGSDERALLDOLHTLLSNTDAGLE 1062
 1072 IDRALGIPELVNOGALERPQDAFQGEAVMDQKAGLYGOTYPAQGPMMO-GGF-HIQ 1129
 1063 IDRALGIPDLVSGQALEPQDPSYOPQSPVMIIDQKRPYGHYAGQAMASAGGFNNMO 1122
 1130 GQSPFNSMNMNM-NQGNFPLQGMHPRANIMPRNTKQRLMQLQRLQGOPLNQR 1188
 1123 GQHPPTVWGMNQOQGMHPRANILIRNNNIRQLMQLQRLQGOPLNQR 1182
 1189 QALEKMENTAGGAIVMRPMO---POGFLNAQVAVRQRELISHFRQORVAMMQO 1245
 1183 QALEKMENTAGGAIVMRPMO---POGFLNAQVAVRQRELISHFRQORVAMMQO 1240
 1246 QO 1305
 1241 QO 1284
 1306 YGNGQPDPAFGVSSPPNANMSSRMGSONPMQHPQALSTIOSSEMGWSPGNTARNS 1365
 1285 YGNGQPDPAFGVSSPPNANMSSRMGSONPMQHPQALSTIOSSEMGWSPGNTARNS 1341
 1366 SFQSOQFAGHGNPNAVYSMVHNSGSHMGOMNPNPMGMPGPOKXC 1415
 1342 SFQSOQFAGHGNPNAVYSMVHNSGSHMGOMNPNPMGMPGPOKXC 1391

RESULT 8
 US-09-125-635-8
 ; Sequence 8, Application US/09125635
 ; GENERAL INFORMATION:
 ; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
 ; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
 ; FILE REFERENCE: 49944
 ; CURRENT APPLICATION NUMBER: US/09/125,635
 ; CURRENT FILING DATE: 1998-08-21
 ; PRIOR APPLICATION NUMBER: 60/049,728
 ; PRIOR FILING DATE: 1997-06-17
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 951
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 ; US-09-125-635-8

Query Match 66.9%; Score 4938; DB 15; Length 951;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 950; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

300 CIOREFSLNDGOSMSOKRHYOEAFLYVHAETPVYRFSIADGTIVTAQRTSKLFRNPVTN 359
 1 CIOREFSLNDGOSMSOKRHYOEAFLYVHAETPVYRFSIADGTIVTAQRTSKLFRNPVTN 60
 360 RHGFVSTHFLQREQNGYRPNPVPVQGITRPMACNSVY-GGMSMSPNOGLQMPSSRAYGL 419
 61 RHGFVSTHFLQREQNGYRPNPVPVQGITRPMACNSVY-GGMSMSPNOGLQMPSSRAYGL 120

QY 420 ADPSTGOMSGARYGSSNIASTLPFGOMOSPSSTYQNNNTGLNMSPPHSGPLAPNOQ 479
D 121 ADPSTTGOMSGARYGSSNIASTLPFGOMOSPSSTYQNNNTGLNMSPPHSGPLAPNOQ 180
QY 480 IMISPRNRSKIXASHOSPAGVHSPMASSGNTGNHSESSSSIALCALISEGVTSLLS 539
D 181 IMISPRNRSKIXASHOSPAGVHSPMASSGNTGNHSESSSSIALCALISEGVTSLLS 240
QY 540 TLSSPGKLDNSPMNNTTQPSKVSNOOSKSPFGYCDONPESSMCOSSNRDHLSDKSK 599
D 241 TLSSPGKLDNSPMNNTTQPSKVSNOOSKSPFGYCDONPESSMCOSSNRDHLSDKSK 300
QY 600 ESSVEGAENOGPLESKCHKLLDLTSSDPRGHSSLTNSPLDSSCKESSVATSPSGV 659
D 301 ESSVEGAENOGPLESKCHKLLDLTSSDPRGHSSLTNSPLDSSCKESSVATSPSGV 360
QY 660 SSSSTGGVSSSTNNHGSLOEKHRLKLLONGNSPAEVAITTAQATGKDRSSTTSCDG 719
D 361 SSSSTGGVSSSTNNHGSLOEKHRLKLLONGNSPAEVAITTAQATGKDRSSTTSCDG 420
QY 720 NVVKEOQLSPKKENNALRYLLDRDDPSDALSKELQPOVEGVNKKMSQCTSTIPSSSQ 779
D 421 NVVKEOQLSPKKENNALRYLLDRDDPSDALSKELQPOVEGVNKKMSQCTSTIPSSSQ 480
QY 780 EKDKRITETSEEGSGDLNDLIDGLTSSDFYNNSSSSNGSHLGTQOYFOGINSGL 839
D 481 EKDKRITETSEEGSGDLNDLIDGLTSSDFYNNSSSSNGSHLGTQOYFOGINSGL 540
QY 840 KSSQSVOSIRPPYNRAYSILDSPVSVSSSPYKNISAFPMPLPKOPMLGPNMMDSOENY 899
D 541 KSSQSVOSIRPPYNRAYSILDSPVSVSSSPYKNISAFPMPLPKOPMLGPNMMDSOENY 600
QY 900 SSMGCPNRYNTVTQTPSSGDMGLPNSKAGMEPMNNSMGRPGGDYNTSLPRALGSGIP 959
D 601 SSMGCPNRYNTVTQTPSSGDMGLPNSKAGMEPMNNSMGRPGGDYNTSLPRALGSGIP 660
QY 960 TLPFRNSIPGARPYLOQOQOQMLMRPEITPMGANCANYGAAASNOICSMRPGDGLSSEQ 1019
D 661 TLPFRNSIPGARPYLOQOQOQMLMRPEITPMGANCANYGAAASNOICSMRPGDGLSSEQ 720
QY 1020 VSHSTONRPLRLNSLDLVPSPNLEGOSEDERALDLHTLTLSTNDATGEIDRALGIP 1079
D 721 VSHSTONRPLRLNSLDLVPSPNLEGOSEDERALDLHTLTLSTNDATGEIDRALGIP 780
QY 1080 ELVNOGQALEKQDAFOQOEAAVMMDOKAGLYGQYPAQGPOMOGGFLQGOSSSFNSMM 1139
D 781 ELVNOGQALEKQDAFOQOEAAVMMDOKAGLYGQYPAQGPOMOGGFLQGOSSSFNSMM 840
QY 1140 NOMNOQGNFPLQGMHPRANITRPRNTPKOLRMOLQOQLQGOFLNOSROALETKMEMP 1199
D 841 NOMNOQGNFPLQGMHPRANITRPRNTPKOLRMOLQOQLQGOFLNOSROALETKMEMP 900
QY 1200 AGGAAYVRPMQPOQGLFNAQVAAQSRRELLSHHFROQRVAMMMQOQOQOQ 1250
D 901 AGGAAYVRPMQPOQGLFNAQVAAQSRRELLSHHFROQRVAMMMQOQOQOQ 951

RESULT 9
US-08-891-640-2
; Sequence 2, Application US/08891640
; GENERAL INFORMATION:
; APPLICANT: Chambon, Pierre
; APPLICANT: Gronemeyer, Hinrich
; APPLICANT: Voegel, Johannes
; APPLICANT: Lutz, Yves
; TITLE OF INVENTION: Transcriptional Intermediary Factor-2
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA

ZIP: 20005-3934
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,640
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,247
; FILING DATE: 12-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1383.0130001/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-891-640-2

Query Match 37.1%; Score 2740.5; DR 12; Length 1464;
Best Local Similarity 42.8%; Pred. No. 1.2e-173;
Matches 644; Conservative 241; Mismatches 435; Indels 163; Gaps 43;

QY 1 MSGLENL-DPLASDRKRLPCDTPGGLGSCSEKRRRDESKYIEELAIISANLSDI 59
D 1 MSGGENTSDPSRAETRRKRCPCDGLSPKRNTEKRRREGENKYEELALIFANFNDI 60
QY 60 DNFVKKPKCAILKETVQIQIKEQCK-TISNDQVQKADVSSTGQVIDKSLGPELL 118
D 61 DNFVKPKCAILKETVQIQIKEQCKAAANIDEVQKSDVSSGQVIDKALGPML 120
QY 119 QALDGLFVNREANIVSENVTOYLQKOEDLVNVSYVNLLEBEDKDLK-LPKEST 177
D 121 EALDGLFVNLEGNVSENVTOYLQKOEDLVNVSYVNLLEBEDKDLK-LPKEST 180
QY 178 VNGSVWNEPOROKSHFNCBMLKTPHDILEDINASEMRORYETMCFALSOPRAME 237
D 181 VNGSMSEPPRRNSHTFNCBMLKTPHDILEDINASEMRORYETMCFALSOPRAME 240
QY 238 EGEDLOSCMTCVARRITTGERTFPSPNPESTFTRHDLGKVVNIDTNSLRSSMRGFEIT 297
D 241 EGEDLOSCMTCVARRITTGERTFPSPNPESTFTRHDLGKVVNIDTNSLRSSMRGFEIT 300
QY 298 RRCIORFSLNDGSSMS-OKRHOEAYLNGHAETPVYFEFLDGTIYAOVKSKLFRNPV 356
D 301 RRCIORFSLNDGSSMS-OKRHOEAYLNGHAETPVYFEFLDGTIYAOVKSKLFRNPV 360
QY 357 TNDRHGEVSTHFLQREONGYRPNPNVQGIIRPMAGCNSSVG-MSMSPQGLQMP 412
D 361 TNDRHGEVSTHFLQREONGYRPNPNVQGIIRPMAGCNSSVG-MSMSPQGLQMP 420
QY 413 SSRAYGLADPESTTGOMSGARYGSSNIASTLPFGOMOSPSSTYQNNNTGLNMSPPHSG 472
D 421 SSRAYGLADPESTTGOMSGARYGSSNIASTLPFGOMOSPSSTYQNNNTGLNMSPPHSG 476
QY 473 LAPNOQNMISPRNR-----GSPKIXASHOSPAGVHSPMASSGNTGNHSESSSSIAL 525
D 477 LAPNOQNMISPRNR-----GSPKIXASHOSPAGVHSPMASSGNTGNHSESSSSIAL 536
QY 526 LQALISEGVGTLSTLSSPGPK---LDNSP-NMNTQPSKVSNOOSKSPFGYCDONPEVE 581
D 537 LQALISEGVGTLSTLSSPGPK---LDNSP-NMNTQPSKVSNOOSKSPFGYCDONPEVE 594

QY 1205 VBRPMPOGFLNAQVARSRELLSHHRRQAVAMMMQ0000000000000000 1264
DB 867 TLAPGV-PTQAPINAOMLQROREILNOHLR-----OQOMHOQOQVOQKRL 911
QY 1265 QOQTOAFSPPPNTASPMGLAGPTMPOAPQOEPYOPNYMGGOQPPAFGRVSSPPN 1324
DB 912 MMHGGGLNTPSVAVASGMPATMSNFRIPQANAOQEPFPNPVGISQOPDGFICATTPQS 971
QY 1325 AMMSMNGSQONPMQHPQAASTIYOS-SEKKGMPGSGNLARNSFSQO---QFAHQGNPAY 1380
DB 972 PLMSPMHATQSPMOOSQONPAYQAPSDINGMAGNMGNSMFSQOSPFPFGQOANTSM 1031
QY 1381 YS-----WYHMGSSGMMGOMNNMPPMPSGM-PMGPDQ 1412
DB 1032 YSNMNNINYSMATNTGMSMNMOTGOISMTSVTSVPTSGLSMGPBQ 1079

RESULT 12

US-09-125-635-2
Sequence 2, Application US/09125635
GENERAL INFORMATION:
APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
FILE REFERENCE: 49944
CURRENT APPLICATION NUMBER: US/09/125,635
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: 60/049,728
PRIOR FILING DATE: 1997-06-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 186
TYPE: PRT
ORGANISM: Homo sapiens
US-09-125-635-2

Query Match 13.0%; Score 957; DB 15; Length 186;
Best Local Similarity 98.4%; Pred. No. 5,4e-56;

Matches 183; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 117 LQALDGLFVVRANIVFVSENVTOYLOQKOEDLVNTSVYILHEEDRKDLKLPKS 176
DB 1 LQALDGLFVVRANIVFVSENVTOYLOQKOEDLVNTSVYILHEEDRKDLKLPKS 60
QY 177 TVNGVSWTNEPQOKSHTECMRLMKTDPHILEDINASPMPORQYETMOCFALSOPRAM 236
DB 61 TVNGVSWTNEPQOKSHTECMRLMKTDPHILEDINASPMPORQYETMOCFALSOPRAM 120
QY 237 EEEEDLOSCMICVARRITGERTFSPNPESFTRHDLSCGVVYIDNLSLRMRPFEDI 236
DB 121 EEEEDLOSCMICVARRITGERTFSPNPESFTRHDLSCGVVYIDNLSLRMRPFEDI 180
QY 297 IRRCIQ 302
DB 181 IRRCIQ 186

RESULT 13

US-08-891-640-3
Sequence 3, Application US/08891640
GENERAL INFORMATION:
APPLICANT: Chamhon, Piere
APPLICANT: Gronemeyer, Hinrich
APPLICANT: Voegel, Johannes
APPLICANT: Lutz, Yves
TITLE OF INVENTION: Transcriptional Intermediary Factor-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/891,640

FILING DATE: Herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/021,247

FILING DATE: 12-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Steife, Eric K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1383.0130001/EKS

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1036 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

US-08-891-640-3

Query Match 11.8%; Score 873; DB 12; Length 1036;
Best Local Similarity 27.7%; Pred. No. 4.1e-49;

Matches 321; Conservative 173; Mismatches 342; Indels 322; Gaps 54;

QY 378 PNPNP-VGGIRPPMAGCNSVGMGSPNQGLQMPSSRAYGLADSTTGOMSGARYGGS 436
DB 4 PRVNPVSINPSIPA-----HGVARSSTLPPSNMNVSTR-----INQOSSDLSSSHSNS 54
QY 437 SNI-ASTLTPGPMQ-----SPSYONNNYGLNMSSPPHSGPGLAPNQONIMISPRN 486
DB 55 SNQSGFSGCSPGQIYANVALNKGAOSSSKPSLNLNPPMGCTGISLAQ---FMSPR 111
QY 487 RGS-----PKASHQSP-VAGVHSPM---ASSGNTGHSFSSSLALQAISEVGRS 536
DB 112 QVTSGLATREPMNNSFPPISTLSSPYGNTSACNNNNNSYNIPVTSLOGNNEGPNNNS 171
QY 537 LLSLSP---GPKLNSPMNITOPSKYSNODS---SPL-----GFCQDNVESS 583
DB 172 VGFSSASSPVLRKQSSONSFRNLIOPAKASKKNEKIASTLNMQSDNSSSGKPLDSG 231
QY 584 MCSQNSRDLSDKSESSVEGAENORGLPESKGRKLLDQLTSCSSDDRRGSSLTNSPLD 643
DB 232 LHHNN--DRISDGSKYSQS-----HKIVQLTTTAEQ---LRHADID 271
QY 644 SSCRESSVYTPSPGVSSSTSGVSSSTSMHGLDQKHRLIKLLQNGSPAFAVAKITA 703
DB 272 TSCKD-VLSCGTGTSNSASANSAGSCPS--HSS-LTARHRLILRLIQEG--SPSDITTLVS 327
QY 704 QATGKDTSTSCGDDNV-----VKQEQLSPPKKE--NNALLRYLDRD-----PSDA 750
DB 328 EPPKDSASTSVSYTQOVQGNSSIKLELDASKKESKQDLRLYLDDKEDKDLRSTPNNS 387
QY 751 LSKELQPOVEGVNKMSSQCTSTIPSSQEKDKIRIKTETSEEGSGDLDNLAIGDLTSS 810
DB 388 LD-DVKVKEKE-QMDPCNTINFTPMTKAPE-EIKLEAQSGTADLDQDQL-----438
QY 811 DFYNNSSISNGSHLGTQOYFGQNTSLGLKSSQSVOSIRPPYKAVSLDPSVSVGSSPPY 870
DB 439 -----438
QY 871 KNISAFPLPKOPMLGPNPMQDSQENYSSMGPNRNVTVTOTPSSGDMGLPNSKAGRN 930

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Db 439 -----PTLEKAAQL---PGICETDR-----MDGAVTSVTKSEITIKSEILPASL----- 480
Qy 931 EPMNSNMGRCGPDYNTSLPRPALGSLPTLELRNSNIPGAPVYQQQQQMLQMRPELP 990
Db 481 ----OSATARP-----TS-----RUNRBP-----ELE 498
Qy 991 MCGMANPYGOAASNOGSPDGMLEMEGVSHGTQNRPLRNSLDIVGPSLEGSDE 1050
Db 499 LEATINOGSGPBTGDI-PWTNN--TVTAINOSKSEDOCISQDELCEPPTVEGRNDE 555
Qy 1051 RALLDQHLTLNSTDATGLEETIDRALGIPELVNOGALPKODAFQGEAA--VMMDOKA 1108
Db 556 KALLEQVLSFGKDETELAEIDRALGIDKLY-QGGGLDVLSERRPPQATPPLMEERP 614
Qy 1109 GLYGCTYPAQGP-----PMCGFHLOGSPSPFSNMNMOM-QQGNF-PLOGMHRPRANT 1160
Db 615 NLYSQPYSSPFTANLPSPFQG---MVROKPSLGTMPVQVTPPRGAFSPGCMQMPROTIN 671
Qy 1161 RPRNTPKOLRMQLOORLOG-QQFLNOSROALELKMENPTAGGAVMRPMQPO---QGF 1216
Db 672 RPPA-APNOLRIQLOORLOGQQLIHONQAI-LNQPATAVGIMNRSGMQOQITPPQP 729
Qy 1217 LNAQVAVOASRELLSHHFROQVAMMMQQQQQQQQQQQQQQQQQQQQQAFSPPN 1276
Db 730 LNAQMLAQORRELYS-----QQHROQLIQQRAMLMRQSGFCNNLPSS 773
Qy 1277 VTASPSMDGLLAGTPPAQAPQOFPYQPNYMGQGPDPDA---FGRVSSPPNAMMSR-- 1330
Db 774 -SGLEVOGT---NPRLPQAGAPQOFPYQPNYGTNPPTPASTSPFSQLAANPASILNRNS 829
Qy 1331 -----MGRSQNPMQH-----P 1342
Db 830 MYSRMTGNTIGGOFSTGILPMQONVFOYPGAGMVPQGEANFAPSLSPGSSVMPPIPP 889
Qy 1343 QA-----ASIYOSSEKMGWPSGNLARSFSO--QOFAHQGNPAVYS--MVHNNGSS 1390
Db 890 QSSLLQPTPPASGYSQSPDKAMQGAIGNNVFSQAVQNPFPAPQGVYNNNSITVSMAG 949
Qy 1391 GHMGOMNNPMPMGMPM 1408
Db 950 GNTVQNMNPM-MAQMOM 966

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APPLICATION NUMBER: 60/003,784
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 220/243
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1061 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-701-154A-5

Query Match 11.8%; Score 872; DB 11; Length 1061;
Best Local Similarity 27.1%; Pred. No. 4.9e-49;
Matches 316; Conservative 174; Mismatches 334; Indels 340; Gaps 52;

Qy 378 PNPNP-VGGGIRPPMAGCNSSVGMSPNQGLOMPPSRAYGLADPTTGQMSGARVGS 436
Db 4 PRVNPVNPSPISA-----HGVARSSTLPSPNSNVSTR---IRQOQSDLHSSHSNS 54
Qy 437 SNI-ASLTTPGPMQ-----SPSSYQNNNYGLNMSPPHSGPLPNOQIMISPRN 486
Db 55 SMSQSGFSGSPSQIVANVALNKKQASSOSSKPSILNLPNPREGICISLAQ---FMSRR 111
Qy 487 RCS-----PKTASHQFSP-VAGVHSPM--ASSGNTGNHSESSSSLSALQAISEGVTS 536
Db 112 QVTSGLATRRPMPNNSFPFNITSLSSPVGMTSSACNNNRYSNIPVSLQMGNEGPNN 171
Qy 537 ILSTLSP---GPKLDNSPNNMINTQPSKVSNDK---SPL-----GFCDDQNPVSS 583
Db 172 VGFSSSPFLROMSSQNSRLNIQPAKESKDNELASTLEMIQSDNSSDGPPLDSG 231
Qy 584 MCOSNSRDHLSDKESKESSEVEGAENQRPLESKHKLLQLLTCCSDDRGHSLTNSPLD 643
Db 232 LHNHN--DRLSQDSKYSQTS-----HKLVQLLTFTAEOQ---LHNADID 271
Qy 644 SSCKESSSVTSPSGVSSSTSGCVSSTSNMGSLLQEKHRIHLKLLQNGNSPAEYAKITA 703
Db 272 TSCXD-VLSCGTSTNSASANSNGSGCSPS-HSS-LTARHKILHRLLOEG-SPSDITTLSTV 327
Qy 704 GATGKDTSSITSCGDGNV-----VKQEDLSPKKR--NNALLRYLLDRDD-----PSDA 750
Db 328 EPDKKDSASTSVYTGVOGNSSTILELDASKKESKHQILRYLLDDEKDLNSTPMLS 387
Qy 751 LSKELQPOVEGVNDKMSQCTSTIPSSQEKDPKIKTETSEEGSGLDNLDAILDGLTSS 810
Db 388 LD-DVKVYKEKE-QMDPCNTPTMTKATPE-EKLEAQSGFTADLDQFQGL----- 438
Qy 811 DFYNNSSNGSHLGTQKQVFOGTNSLGLKSQSVQSTIRPPYNAVSLDSPVSGSSPPV 870
Db 439 ----- 438
Qy 871 KNISAFPMLPKQPMLGPNRMMDSENYGSSMGCPNRNVTYQTPSSQDWMGLPNKACRM 930
Db 439 -----PTLEKAAQLPG-----LCETDRM 456
Qy 931 EPMNSNMGRCGPDYNTSLPRPALGSLPTLELRNSNIPG-----APRVLQQQQQMLQ 984
Db 451 D-----GAVTSVTKSEILPASLQSAFTARTRLN----- 486
Qy 985 RPELPMCGANPYGOAASNOGSPDGMLEMEGVSHGTQNRPLRNSLDIVGPSNL 1044
Db 487 RLPELELEIDNQFOGPGTGDQI-PWTNN--TVTAINOSKSEDOCISQDELCEPPTTV 543
Qy 1045 EGOSDERALLDQHLTLNSTDATGLEETIDRALGIPELVNOGALPKODAFQGEAA--V 1102

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Db 544 EGRNDEKALLEQVLSFGKDETELAEIDRLGIDKLV--QGGGLDVLSEFPPOQATPPL 602
 QY 1103 MMDQKAGLVGQYTPAGP-----PMGGFHLQGSFSPFMSMNQNM--QOQNF-PIQGMH 1154
 Db 603 IMERNLTSQPYSSPPFANLPSPPQG--MYRQKPSLQTMVQYTPRGAFSPQGMQ 659
 QY 1155 PRANIRPPTNTPKQLRMQLQQLQRLQ--QOFLNQSROALELKMENPYAGCAVVRPMMPQ 1213
 Db 660 PROTLMRPPA-APNQLRLQQLQQLQQLQQLQQLQQLQQLQQLQQLQQLQQLQQLQQLQ 717
 QY 1214 ---QGFANQVAQKRSRELLSHHFROQRYAMMMQ0000000000000000000000 1270
 Db 718 ITPQPLNQAQMLAQRLQRLQRLQRLQRLQRLQRLQRLQRLQRLQRLQRLQRLQRLQ 761
 QY 1271 FSPFPVNTASPSMDGLLAGPTMPOAPPOQFPYQNTGKQOQPPA----FGRVSSPPNM 1326
 Db 762 NNLPSP-SGLPQVGT--NPRLPQAGAPQOFPYPPNTGTPGTPASTSPSOLAANPEAS 817
 QY 1327 MSSR-----MGPSQNPMMQH-----1341
 Db 818 LANRNSMVRGNTGNIGGQGTGCTINPOMQONVQYPGAGNVPGCANFAPSLSPGSSMVP 877
 QY 1342 ----PQA-----ASTYQSEMKGWPSSGNIARNSSFSQ--QOFAHQGNPAVYS--MY 1384
 Db 878 MP1PPOSSILQOTPPASGYQSPDKAMQOQAGINNNVFSQAVQNOPTPAQPGVYNNMSI 937
 QY 1385 HMGSSGHMGOMNMNPMPSGMPM 1408
 Db 938 TVSMAGNTNVOMNPM-MAQOMQ 960

RESULT 15

US-60-236-359-19468
 ; Sequence 19468, Application US/60236359
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: MDHORE-4P
 ; CURRENT APPLICATION NUMBER: US/60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; NUMBER OF SEQ ID NOS: 21709
 ; SOFTWARE: Molecular Dynamics Sequence Listing Engine
 ; SEQ ID NO 19468
 ; LENGTH: 149
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AL034418.2
 ; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.1
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
 ; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 2.1
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
 ; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
 ; OTHER INFORMATION: EST_HUMAN HIT: AM503706.1, EVALUATE 9.00e-51
 ; OTHER INFORMATION: SWISSPROT HIT: Q58434, EVALUATE 5.30e-01
 US-60-236-359-19468

Query Match 10.1%; Score 742; DB 23; Length 149;
 Best Local Similarity 99.3%; Pred. No. 8.6e-42;
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 644 SSKESVSATSPSGVSSSTSGGVSSSTSNMHSLLQEKHRIHLKLLONGNSPAEVAKITA 703
 Db 1 SSKESVSATSPSGVSSSTSGGVSSSTSNMHSLLQEKHRIHLKLLONGNSPAEVAKITA 60
 QY 704 QATGKDTSSITSCGDNVYKQEQLSPRKKENNALRYLLDRDDPSDALSKELQPOVEGYD 763
 Db 61 EATGKDTSSITSCGDNVYKQEQLSPRKKENNALRYLLDRDDPSDALSKELQPOVEGYD 120
 QY 764 NKMSQCTSSITPSSSQEKDPKITEETSEE 792
 Db 121 NKMSQCTSSITPSSSQEKDPKITEETSEE 149

Search completed: April 19, 2001, 16:54:00
 Job time: 487 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2001, 16:45:56 ; Search time 7.55 Seconds
(without alignments)
474.448 Million cell updates/sec

Title: US-09-041-994-2

Sequence: 1 MSGIGENLDPLASDSRRKRL.....NMNMPMSGMPDPDQKYC 1415

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 12259 seqs, 2531507 residues

Total number of hits satisfying chosen parameters: 12259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/prodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/prodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/prodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/prodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	3.5	826	US-09-533-077-330	Sequence 330, App
2	189.5	2.6	849	US-09-792-024-119	Sequence 119, App
3	166.5	2.3	1355	US-60-248-505-1205	Sequence 1205, App
4	165	2.2	1503	US-09-649-996-14	Sequence 14, App1
5	163	2.2	3418	US-09-421-124-44	Sequence 44, App1
6	163	2.2	3418	US-09-421-124-44	Sequence 44, App1
7	161	2.2	1833	US-08-945-567C-4	Sequence 4, App1
8	161	2.2	1992	US-08-945-567C-3	Sequence 3, App1
9	160.5	2.2	782	US-09-739-449-11432	Sequence 11432, A
10	158.5	2.1	2329	US-09-421-124-16	Sequence 16, App1
11	158.5	2.1	2329	US-09-421-124-16	Sequence 16, App1
12	155	2.1	2128	US-60-248-505-927	Sequence 927, App
13	151.5	2.1	884	US-60-248-505-690	Sequence 690, App
14	147.5	2.0	1206	US-60-248-505-1161	Sequence 1161, App
15	147	2.0	2000	US-60-248-505-714	Sequence 714, App
16	145.5	2.0	583	US-09-810-264-38	Sequence 38, App1
17	140.5	1.9	1067	US-60-248-505-1184	Sequence 1184, App
18	140	1.9	1005	US-09-812-471-1	Sequence 1, App1
19	140	1.9	1005	US-09-812-471-1	Sequence 1, App1
20	138.5	1.9	1791	US-60-248-505-871	Sequence 871, App
21	136	1.8	1044	US-60-248-505-860	Sequence 860, App
22	135	1.8	1234	US-09-739-449-8719	Sequence 8719, App
23	134.5	1.8	1579	US-09-421-124-184	Sequence 184, App
24	134.5	1.8	1579	US-09-421-124-184	Sequence 184, App
25	133.5	1.8	1002	US-09-812-471-3	Sequence 3, App1
26	133.5	1.8	1002	US-09-812-471-3	Sequence 3, App1
27	133	1.8	1384	US-09-649-996-11	Sequence 11, App1

28	132	1.8	4044	US-60-248-505-791	Sequence 791, App
29	131.5	1.8	1535	US-09-421-124-185	Sequence 185, App
30	131.5	1.8	1535	US-09-421-124-185	Sequence 185, App
31	128.5	1.7	782	US-09-813-408-29	Sequence 29, App1
32	128.5	1.7	1471	US-09-421-124-188	Sequence 188, App
33	128.5	1.7	1471	US-09-421-124-188	Sequence 188, App
34	128	1.7	1228	US-09-661-222A-38	Sequence 38, App1
35	126.5	1.7	1494	US-09-421-124-186	Sequence 186, App
36	126.5	1.7	1494	US-09-421-124-186	Sequence 186, App
37	119	1.6	2031	US-09-739-449-10349	Sequence 10349, A
38	116.5	1.6	681	US-09-336-910A-2	Sequence 2, App1
39	116.5	1.6	1915	US-60-248-505-688	Sequence 688, App
40	113	1.5	560	US-09-810-264-10	Sequence 10, App1
41	112.5	1.5	543	US-09-533-077-337	Sequence 337, App
42	111.5	1.5	886	US-09-739-449-10232	Sequence 10232, A
43	110.5	1.5	3170	US-60-248-505-909	Sequence 909, App
44	110	1.5	1683	US-09-421-124-183	Sequence 183, App
45	110	1.5	1683	US-09-421-124-183	Sequence 183, App

ALIGNMENTS

```
RESULT 1
US-09-533-077-330
; Sequence 330, Application US/09533077
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C5
; CURRENT APPLICATION NUMBER: US/09/533.077
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ. ID NOS: 800
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-077-330
```

Query Match 3.5%; Score 258; DB 5; Length 826;
Best Local Similarity 19.8%; Pred. No. 1e-09;
Matches 181; Conservative 136; Mismatches 320; Indels 278; Gaps 41;

```
QY 1 MSGIGENLD--PLASDSRRKRLPDDTGGGLTSGGRRRQESKYTEELAEISANLSD 58
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MEGAGGANDKKRKISSERREK-----SRDARSRSKESEVEYELAH----OLPL 46

QY 59 IDNENVPDCAIKKEIVR--QIROIKEOGKTISDNDVQKADVSSGGQVIDKDSGLP 116
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 47 PHNWSHLDRASVRLITSLRVKLLDAG--DLDIEDM-----KAQNCVF 91

QY 117 LQALDGLFLEPVNEANIVFVSENVTOYLOYKQBDLVNTSVYNIHBEDEKDFLKNLPS 176
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 92 YLKALDGFVMLTFDDGMITYSDNVKMYGLQTELGHSVFDFTHPCDHHEMKMLTHR 151

QY 177 TVNG-VSWTNEPQOKS-----HTFNC-----RLMKTYHDLIEDINAPDEM 217
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 152 --NGLVKKRGEQNTQSFLLRMKCTLSRGRTNKAISATKVLHCTGHIVYDTNSNP- 208

QY 218 RQRETFMOCFALSPRAMEEGEDLOSCMICVARRITTGERTFSPNDE-----SFTTRH 271
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 209 -----QCGYKRP-----MTCVILICPI-----PHRSNIEIFLDSTFISRH 246

QY 272 DLGKVVNIDTNSLRSSMRPGF--EDIIIRCIORFFSLNDGQSWQSRKHYQOAYLNGHAE 329
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 247 SLDMKFSYCDK---RITELMGYPEEDELGRSIVYVHALSDHILTKYHH--DMFTKGQV 301
```


LENGTH: 1355
 TYPE: PRM
 ORGANISM: Human
 US-60-248-505-1205

Query Match 2.3%; Score 166.5; DB 6; Length 1355;
 Best local similarity 17.9%; Pred. No. 0.0012;
 Matches 265; Conservative 111; Mismatches 510; Indels 535; Gaps 64;

QY 10 PLASDRKRLPCDTPGEG--LTCGSEKRRRDE-SKYELELAELISANLSDIDNENVRK 66
 DB 211 PMAG-SKTSSTPERKODEKEISOEGDEPARQSVSKIRDOFGQ-EGNLA----- 259
 QY 67 DKCALIKETVROIRKQKQKTSINDDDVAKADVSSSTGCGVIDKDISGPIILLALDGLF 126
 DB 260 TOSPPREAVORPCEDDETCKSTDSKDVCRMPDIOEPGKADQTPATKMLGEPED--- 315
 QY 127 VVNRANIVSEENVTOYLQKQEDL-VNITSVYNILHEEDRKDFLKNLPKSTVNGVSWTN 185
 DB 316 -----YGRSTGEKCEKCKDLFVYQSGRRGSETSDMRDERKRRRQPEAHGTAQOK 366
 QY 186 EPORQSHTEFCMLMKTPIHLEDINASPQMORYETMOCFALSDPRAMEGEDLOSC 245
 DB 367 ERDRKWL-----VLE---TOTQCKYQELQGLSKDAEKSETOYLLS- 407
 QY 246 MICVARITIGERTFP-----SNPESFITRDLGSKVYNIDNLSRSMRGFEIIR 298
 DB 408 -----EGGDDTHPELEGTAVSGEAEHTKEGTAEAFVN-----SKNAPAAE- 448
 QY 299 RCIOREFSLNDGWSOKRHYOEAYLINGHAETPYRRESLADGTIVTAQTSKLEFRNPTN 358
 DB 449 -----RTLGARETQDL-----APLEKOSVGEENTVY-----KTHDOVY- 482
 QY 359 DRGFEVSTHLOREQNCYRPNPNVGGIIRPMACNSSVGVGMSMSPNOGLOMPSSRAYG 418
 DB 483 -----EEDDQY-----QG-EDPESPFTQDEGSESETPNS----- 510
 QY 419 LADPTTGOMSGARYGSSSIASITPGRGMOSSSYONNNG-----LNMSSPHGS 470
 DB 511 -----LASEEGSSSETGELP--VOGDSQSGDGHGSEVGGHNNNPOTROGT 557
 QY 471 PGLAPNOQINIMISPRNG-----SPKIASHQ-----ESPAYGVH---SPMASSGNT 513
 DB 558 PG-EKNNALEAVYPVAVGEVQVLTEDEQPRREHKNQPGTKRGCAAEVPHGHPAOSTA 616
 QY 514 GHSFSSSSLSALOISEGVGTSLLTSSPGPKLNSPNNMTTPOPSKVSNOQSKSPLEFG 573
 DB 617 GDBNRKSLTEITGALDEDF-TDOLSLMQLPG-KGDSRNELKVOGFS----- 661
 QY 574 YCQONPVESSMCSNSNDHLSDEKSESSVEGANONGRPLESKGHKLLQLLTCCSDRG 633
 DB 662 -----SKEEGRATEAO----- 673
 QY 634 HSSLTNSPLDSCKESSSVTSPGVSSTSGVSSSTNMHGSLLQEKHRLHKLLONGN 693
 DB 674 -----HTLESLEDBDNASLX-----IOLEKTEPVTSE-----EED 705
 QY 694 SPPEAKITTAQATGKDTSSITSCGDGNVAKOEOLSPKAKKNNALLRLYLLDRDDPSALSK 753
 DB 706 SPOELA-----GEGG-----DQKSPAKKEHNSV-----PMSLEK 736
 QY 754 ELQPOVGVNKKMSQCSSTIIPSSQEKDKKITETSEBSSGDLNDLILGLTSDXY 813
 DB 737 QMRDOPCPCSVGAVYSSPLYOYLQKLIQQTNVQEEHQVO-----TAQASGELC 791
 QY 814 NNSISSNGSLGTQOQVQCTNSLGLKSSQVOSIRPPYRAVSLD-SPYSGVSSPPV-- 870
 DB 792 SVSLTSLISDC-----SVFFNYSOASQ-----PYTRGLPLDPSPAQAQETPAQA 836
 QY 871 ---KNIS-----AFPN-----LDPKOP 883
 DB 837 LEDKOVSSVHNSLKGNSLSVFCSMFRRRSWPCRHOPACLVREAFPAAGRAHPAPAVPR 896

QY 884 MLCGNPRMDSOENYSSM-----GGPNRVTV---TQPS-----SGDWGLPNSKAGME 931
 DB 897 IYGRFFLLENKQHLGSEFVYRWMDGAPMLCLIPRNTGTQORVLPVYVSPSKKPEVLS 936
 QY 932 PMNSNSMG-----RPGDDYNTSLP---RPAIGSIPPLPLRSNSIPCARPYLQOQOQ 980
 DB 957 ACSNMMGHLSPVRIPLRCKFNQLPSLDEQVYIPALPMVEVRAEPRKATEVKQOVET 1016
 QY 981 MLOMRGEIIPMGKANDPYGAAASNOL-----GSPDGMLSMEOVSHGTONRPLRN 1032
 DB 1017 Q-----GOENKRRPCSCNGEAASTSLFTQGNLTSSWY----- 1051
 QY 1033 SLDDLVGPPNSLQOSDERLLD-----QLHTL-----LSNTDQGLDET--- 1072
 DB 1052 -----PRLBGNVHLKSLIEKNQTDKAQVHAVSFYSKDHEVASHSPAGGLPFGPK 1103
 QY 1073 -----DRALGIPELVNOGOALEPRKDAFGQ-----Q 1098
 DB 1104 DPLPTVLPAPVPGCSLMPEKALKVLGKDLHLPSPSGLLMVGEDMQPKDPALASSRSSPS 1163
 QY 1099 EAAVMDQKAGLYGQYTPAAGPPMGGFHLQGSFSPNSMMNNOQG---NFPLOGMH 1154
 DB 1164 RAASHSSHKRKL-----SEPLQ-----LOPTPP---LOLKMDDRGCPPPAKFPCC--LS 1207
 QY 1155 PRA---NIMRPTNTKOLRMLOQLQOQFL-----NOSRALELKMENPT 1199
 DB 1208 PEALTEKRLKRNKTLIMVIASEKSKRESGETVYVKEVLDIKKWRDPCKDKDKODSK 1267
 QY 1200 AGCAAVMRPMQPOGFLANQMVAVORSRELSHHFRQOVRAMM00000000000000 1259
 DB 1268 AGNOTKKKROOTDQ-----SRESQDLMRHVRQO-----LPTPSDDSHGVKAHNOE 1314
 QY 1260 QOQOQOQOQOAFSPP-----NVTAS---PSMDGLLAGPT 1291
 DB 1315 SOHTRRHQVRLDSPEONIGRHQVTOGAQIPLNSNGAKGET 1355

RESULT 4
 US-09-649-996-14
 Sequence 14, Application US/09649996
 GENERAL INFORMATION:
 APPLICANT: Jono, Keith E.
 TITLE OF INVENTION: KINASE GENES AND USES
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/649, 996
 FILING DATE: 29-Aug-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/976,255
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 229/182
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1503 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 US-09-649-996-14

Query Match 2.2%; Score 165; DB 5; Length 1503;
 Best Local Similarity 20.9%; Pred. No. 0.0017;
 Matches 222; Conservative 136; Mismatches 383; Indels 322; Gaps 57;

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OY 2 SGLGNLPLASDSKRRKRLPCD-----TPGGLTCSGGEKRRRQESKYIEELAEI-- 51
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 600 SSTDEDFQSSSTDPKDSSLPGDLHVTSGPESPNNIFNDVDSEDLPSHOKIFDLMELNG 659
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 52 ISANL-----SDINFNVPKPKCALIKETVROIQIKEOGKITSNDVDYAKAVYSTGQ 105
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 660 VQADKRPATLSSLDN-----PKESVITGHPEKEKPKKIFDSEPLCLSD----- 703
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 106 GVIDKDSIGPLLLQAL-DGFLFVNREANIVFVSENNYQYLOYKQEDLVN-----T 155
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 704 NLMHODNDPDLVNOQLSENFLEL-QEKRLKGLSKSKHEINDLQTELKNAQFTAMLET 761
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 156 SVYNIHLHEDRKDFLKNLPKSTVNGVSWTNEPQROKSHTFNCRMLKTPHDLIEDINASP 215
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 762 SCRNLDLDE--LQFAENRP-----GLSLQENVSTKGDGTD--VMLTGDTLSTLSQSSP 811
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 216 EMR---QREYETMQCALSQPRAMEEGEDLQSCMICVARITTGERTPEPSNPEFTRND 272
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 812 EVQVPTSEFETETRRRVPDLSLPTQGETPCLDIV-----PEDCL-HQD 857
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 273 LSGKVVNID-----TNSL--RSSMRPG-FEDIIIRCIQRFSLNDQGSWSQKRHYQ 320
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 858 ISPDVAVTPELITSDARTSHLSDNRSDSPGSEFELR-----LTFESDS----- 901
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 321 EAYLNGHETPYRFSLADGTVT-----AOTKSKLFRNPVNDIRGFVSTHFORE 372
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 902 -----VLADDLIASRVSVGSSLPELGOELHNKPFSEDDH--SHRLEKN 943
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 373 QNGYRPNPNVQGIIRPPACGSSVGVGMSMSPNOGLOWPSSRAVGLADPS--TTGQMSG 430
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 944 LEAVE-TLNQLNSKDAAEAGLVSLSDSTSQDSLSDLSAPPASPEPSLETDSLES 1002
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 431 ARYG-----GSSNIASLTPGPGMQSPSSYONNNYGLNMSSP-----PHGS----- 470
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 1003 VDVEHALDLSGSHTPQKLV-PDKPADSGYTE---NLSPENTLHPAPRGTADESPA 1057
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 471 -----FGLAPNOONIMISPRNKGSPKIASHQFSPVAGVHSPMASSGNTGHSSTSSSL 523
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 1058 TTGDGSHGLPRNPV-IVISAGDD-----HRGTEVTPETFTTASQGSYRPSAFAFSDND 1110
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 524 SALQAISEGV-GTS-----LSTLSSPGPKL-DNSPNNMNIQPSKVVNODSKSPGLGFC- 575
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 1111 SEPEKRESEEVPTSPSALVLYVOEQLPPEVLPREGSP-----AAQDS-----CL 1153
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 576 ---DQNPVESSKQGSNRDHLSDKESKSSVGAENQRPLESKHK--KLLQLLTGSSD 630
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 1154 EARKSQPDESCISALHNSSDELRTATPEPAGVPOQVHPREDEASSPMVYLNALSSSD 1213
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 631 P-----RGHS-----SITNSPDDSSCKESS-----VSTSPSG 658
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 1214 DFETQDDRPCTLASTGTNTNELLATYNSALDKSLSSHSEGPXKLPDIEGKYLGLGVSG 1273
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 659 VSSSTSGGVSS---TSNMHGSLLQEKHRLKLLQNGNSPAP--VAKITPAQATGKDTSSI 713
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 1274 MLDLSEGDMDADEDENDSDDEDLRAFNLSLSSESEDETEHPVPIILSNEDGRHLSNL 1333
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

```

OY 714 ---TSCGCGNVVKQQLSPKKKENNA-----LTRYLLDRDDPSDLSKELOP---QVEG 761
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 1334 LKPTAANAPDPLPEDM-----KKKKAATVFEDDVLYLFQGETP-----TKELGPGCGEACG 1385
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 762 VDNK-----MSQCTSSITPSSSQEKPKITETSEBSG-DLONLDAIIGDLTSS 810
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 1386 PDLGSPAPASGPYLSRCTNS-----ESSYDEEGGGEWDD----- 1421
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 811 DFYNNSSISNGSHLGTQKQVFOGTNSLGLKSSQVSQIR---PPYNRAVSL---DSPV 862
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 1422 DESPPDFMS-----TTSNLLSKRPSLQTSKYFSPPPARSTRQSWPHSAPY 1468
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 863 SVGSSPPVKNISAFPPMLPKQPMGLGNPRMDSQ-ENYSSMCG 904
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 1469 SFSISPA-NIASFSL-----THLTDSIDRQGSSEDDG 1500
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

RESULT 5
 US-09-421-124-44
 Sequence 44, Application US/09421124

GENERAL INFORMATION:

APPLICANT: Futreal, Phillip A

APPLICANT: Wooster, Richard F

APPLICANT: Ashworth, Alan

APPLICANT: Stratton, Michael R

TITLE OF INVENTION: Materials and methods relating to the

TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer

TITLE OF INVENTION: susceptibility gene and uses thereof.

NUMBER OF SEQUENCES: 222

CORRESPONDENCE ADDRESS:

ADDRESS: Bell Seltzer Park & Gibson

STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107

CITY: Raleigh

STATE: NC

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (ERO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421,124

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/755,587

FILING DATE: 25-NOV-1996

APPLICATION NUMBER: GB 9523959.6

FILING DATE: 23-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9617961.9

FILING DATE: 28-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Kenneth D Sibley

REGISTRATION NUMBER: 31,665

REFERENCE/DOCKET NUMBER: 5405-135

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 3418 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-421-124-44

Query Match 2.2%; Score 163; DB 5; Length 3418;

Best Local Similarity 17.6%; Pred. No. 0.0067;

Matches 251; Conservative 195; Mismatches 480; Indels 500; Gaps 60;

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OY 7 NDLPLASDSKRRKRLPC-----DTPGGLTCSGGEKRRRQESKYIEELAEIISAN 55
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

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Db 1333 NLEFDGSSKNDTVCIHKEDTDLFTDQHNICKLSGQ-----FMKEGNTQIKED 1393
QY 56 LSDIDNENVPADKCALIKETVROIQIEQKTTISNDDDYOKADVSTGGVIDKDSLGP 115
1384 LSDLTLELV-----AKQGEACHGNTSMKEBOLATKTEONIKDEFTSPT----- 1426
QY 116 LLIQALDGLFVYVREANIVFSEVNTQYLOKQEDLVNTSVYNIILHEEDKDEKLNILPK 175
1427 -FTQTSAGKNISVAK-----LFNKIVNFFDQKPEELHNSFLNSHLSIDIRKNKMDILSY 1480
QY 176 STYNGVSWTEPQROKHTENCRLMKTPIHDIILEDIINASEMRORYETMOCFALSOPRAM 235
1481 EETDIYA-----HKILKE-----SVP--- 1496
QY 236 MESEEDLOSCMICVARITTEGR--TEPSNPE-----SFIRHDLGKVVNIIDNSL 285
1497 -----VGVGNQLVTFQOGPERDEKIKEPTLIGFHASGKVKVIAESL 1539
QY 286 RSSMRGFEETIRRCIORFSLNDGOS-----MSOKRHYOAYLVNGHAETPPVRFSL 337
1540 -----DKVKNL-----FDEKEGTSEITSFSHOWAKTLKREACKD-----LEL 1578
QY 338 ADGTI-VTAQTKSKLFPNPTNDRH-----GFVSTHFLQREON-----GYR 377
1579 ACETIETTAAPKCKEMQNSLNNDKNLVIETVPPKLLSDNLKROTENLTKTSKIFLKV 1638
QY 378 PNPVYOGGIRPPMACNSSVVGKSMSPNOGLQWSPRAYGLADPST----- 425
1639 VHENVEKETAKSP-ATCYTQSPSYTIENSALAFYTCSSKRTSVSQTSLLEAKKWLREGI 1697
QY 426 --GQ---MSGARYG-----SSNIAS-----LTPGQMOSPSSYONNNGYLNMSPP 467
1698 FDCQPERINADYVGNLYENNSNSTIAENDKNHLSKQTYLNSNSMSNSYSVHSEVY 1757
QY 468 HGSPGLAPNOQNMISPRANGSPKIASHOPSPAVGHSPPMASSANTGNHSF-----SS 521
1758 NDRITLISKNLD-----SGIEPVKNVEDQONTSPFSKVISNVKD 1796
QY 522 SLALQAISEGVTSLSTLSSPCP-----KLDSPPMNITOPS----- 560
1797 ANAYPOVNVNDICVEELVYTSPPCKNKNAIKLSTISNPNFEVGPFPRIASGIRLCSH 1856
QY 561 ----KVSNDOSKSPPLGYCDQNPVSSMCQ-----SNSRDLSDKES-KESSVEGAENORG 611
1857 ETIKKVIDIDFSKVLFTKENNENKSKICQTKMACYEAALDSEDIHNSLDNDE---- 1912
QY 612 PLKSGKKKLLQLLTSCSDRGHSSSLTNSPLDSCKSSSVTSPPSSVSTSGGVS-ST 670
1913 -CSMHSKVFADI--QSEBILQHNOMSGLE-----KVKISIPCDVSLTSDICKCSI 1962
QY 671 SNHGSILQEKHRLHLKLLQNGNSPAEVAKITAQATGKDTSSITSCGDGVNVQEOLESPK 730
1963 GKHLKSY-----SSANTCGIFTSASGS-----VOYSDASLQNAKROVFE 2002
QY 731 KKEN--NALLRYLLDRDPDSALSKELOPYEGVDNKMQO-----CTSSITP--SSSQ 779
2003 IEDSTKQVFSKVLFEKSNHSDQLTRENTALRIPEHLISQKFSYVNVNSANSRGEFTAS 2062
QY 780 EKRPKIKTIESESGDDLDMLDALGD-----LTSDFYNNSTISSGSH 823
2063 GKQVSTLESSELAHKVGLFEFDLIRTEHSLHYSPTSRONYSKILPRYDKRNPHECVNSEM 2122
QY 824 LGTKOOVFOGTNSLGLK--SSOSVOSTIR-PPYRBAVSIDSPPVSGSPPKNISAPFMLP 880
2123 EKTKSKEFKLSNNLVNVEGGSSENNHSTIKVSPY-----LSQFOQDK 2162
QY 881 KQPMLGPNPMMDQSENYGSSMGCP--NRNVTYVOTPSSGDWGLPNKAGHMEPMNSN--- 936
2163 OQVLGTVKSLVENIHVLGEQASPKNVKMEICKTEFTSD-----VPYKTIIEV 2211
QY 937 --SMGRGGGYNTSLRPAALGGSIPITPLRSNNSIPGARPVYLQOQOQMLQMRPGEIIPMGK 994
2212 CSTYSKDESENY-----FETEAVEIAKAFMEDD-----ELTDSKLP--- 2246

QY 995 ANPYGAASNOLGSMWPDG---MLSMEOVSHGTONRPLRLNSLDLYGPPS---NIEGOS 1048
2247 -----SHATSHLFTCEBNEEMVLSNRSRICK-RGGEPLI-----LVGEESIKRNL----- 2289
QY 1049 DERALLDOLHTLLSNTDATGLEETIDRALGIPELVNOGALPEKODAFQGOEAAVMDOKA 1108
2290 -----LNEFDRI-----IENQKSLKASKSPDQ-----TIKDRLL 2320
QY 1109 GLYQOTYPAGCPMGOGFPHLOGSPFSFNSMMQNOGNEPPLQCMHPRAIMPTRTYPK 1168
2321 FMH-----HV-----SLEPITCVPEFRTKEROEIONPNTAP- 2352
QY 1169 QLRMLOQRLOGOFLNOSRQALTEKMENTPAGGAAYMRPMOPOQGFELNAQVYARSRE 1228
2353 -----GOEFLSKSHLHEHLETKSSSNLAVSGHPFYQ-----VSATRNE 2391
QY 1229 LLSH-----HFRQOYAMMMQOQOQOQOQOQ 1255
2392 KMRHLITTGRTKVFVPPFKTSHF--HRYEQCYRNINLEENRQK 2435

RESULT 6
US-09-421-124-44
Sequence 44, Application US/09421124
GENERAL INFORMATION:
APPLICANT: Futreal, Phillip A
APPLICANT: Wooster, Richard F
APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer
TITLE OF INVENTION: susceptibility gene and uses thereof.
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CITY: Raleigh
STATE: NC
COUNTRY: USA
ZIP: NC 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,124
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3418 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-421-124-44


```

Db 692 TSANGTATN-----FNVSDEDALVNAKDIAENLTLAKEIHTTKGTAADTALQT 742
Oy 227 FALSOPRAMEBEDQSCMICVARITTEGRTFPPSNPEFTRHDLSCVAVIDTN--- 283
Db 743 FTVYK-----VDENNNDADD-----ANATVGOQN-ANNQVNTLTLKENGINTIDKNGTV 792
Oy 284 -----SLRSSMRPGFEDIRRCIORFSLNDG-----OSMSQRHYOEAYLVNG 326
Db 793 TEGINTTSLGAKKS-----TLNDGGLSTKNPFGSEIOVGADGVKAKYNNNG 841
Oy 327 HAETPVRESLADGTIVTAQTSKLEFRNPVYNDRHGFVSTHFLORONGY--RPNPNVYG 384
Db 842 VVGAGI-----DGT-----TRITREIGFTGT-----NSGLDKSKPHLSK 876
Oy 385 QGIRPMAAGNSVGVGMSPNGLDMPSSRAYGLADPSTTGOMSGARKGSSNINSLP 444
Db 877 DGI-----NAGGKKTITNIOGEL---AONSHDAVYGKIYDLKTELEKRISS-7A 922
Oy 445 GPGMOSPSY-----ONNNYGLNMSSPHGSPGLAPNO-----ONIMISPRNGSPKI 492
Db 923 KTAONSLHEFSVADBOGNFTV---SNPYSSYTSKTSVYITRAGENGITTKYNNKGVYR 979
Oy 493 ASHOFSPVAGVHSPMASSGNTGNHSPSSSLALQAISEGVGTSLSTLSSPGPKLDNSP 552
Db 980 GIDQ---TKGLTTPKLTGVNNGKGIVIDSONCONITIT-GLSWTLANVTNDKG----- 1028
Oy 553 NMNITOPSKVSNODSKS-----PLGF-----YCDONPVESMA 564
Db 1029 SVTTEOGNLIKEDKTRAAIVDVLISAGFNLOGNEAVDFVSTYDTPVNDADNATYAKV 1088
Oy 585 COSNSRDLSDKESKESSEVEGAEN-ORGPLESKHKLLLOLTCSSDDRCHS--SITNSP 641
Db 1089 TY-----DOTSKTSKYVYDVNVDITIEVDKLGVTTLTLTSTGICANFALSNOA 1140
Oy 642 LSSCKESSVSVTSPGVSS--STSGVSSSTNMHGSLLQEKHRLHLKLLONG----- 692
Db 1141 TGDALTKASIDIVAHNLTLSDIQTAKGASQANNAGVADADGKVIYDSTDNKYQAKND 1200
Oy 693 ---NSPAEVA--KITAOATGKOTSSITSGDGVVVOEOLSPKK-----ENNALRLYL 742
Db 1201 GYVDKTRKFAKDLVAOQTPD--GTLOAMNKVINKIEOVANDANKOGINEDNAFYKGL- 1258
Oy 743 DRDDPSLASELQOPEGVGNKMSQCTSTIPISSOEKPKI-----KTESSE-- 791
Db 1259 -EKAADNKTNAAYTV-GDLNAVAO-TPLTFAGDGTTRAKKIGELITITKGGOTDNKLT 1315
Oy 792 -----EG-----SGDLNLDAILGDJTSSD-----FYNNS-----ISSNGS 822
Db 1316 DNNIGVAGIDGFTYKLAQDLTLNLSVNAAGTKIDKGVSFVDSGQAKANTPVLISANGL 1375
Oy 823 HIGTK---QOYFOGTSLGLKSSOSVOSIRPPYKRAVSLDSPVSGSPPKNISAFPMPL 880
Db 1376 DLGKVIISVNGKGTJTDANVOOLEVNR-----NLGLGNAQDNADNOVNIADIK 1428
Oy 881 KOPMLGPNPMMDSOEYSSMGCPNRNVTVTQTP-----SSGD-----MGLPN 924
Db 1429 KDNSSSSSNR--TVIKAGTVLGGKGNDEKATGCIQVGVCKDGNANDLSNMV-VKT 1485
Oy 925 SKAGREPM--NSNSMGRPGDYNTSLPRPALGSIPTLPLRSNSIPGAR----- 972
Db 1486 OKSGSKALLATAYNAAGOT--NYLTNNPAEALD-----RINE-OGIRFFHVNDGNOE 1534
Oy 973 PVLQOQOQMLQMRPE--IPMGANGPYGOA-----ASQOLGSWPDGMLSM--EOY 1020
Db 1535 PVOQGRNGIDSSASGRHSAVIGFOAKADGEAAVAIGROTQAGNOSIAIGMAOATGQOSI 1594
Oy 1021 SHGTRPPLIRNSLDLVGPPSLLEGOSDERALLDOLHTLNS---TDATGELDEIRALG 1077
Db 1595 AITGTM--VYAGKHSAGLIDPSTYKA-----DMSYSGNNNOFTDATTQTVFVGANN 1644
Oy 1078 IPELVNOGALPEPKODAFQOEAAVMMDOKAGLYGQTYRAGPMPMGCF 1126
Db 1645 ITVETESNVALGSNSAISAGTHAGTQAKKSDGTAGTTTATGATGYKGF 1693

```

```

RESULT 8
US-08-945-567C-3
; Sequence 3, Application US/08945567C
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
; FILE REFERENCE: 1038-745 MIS
; CURRENT APPLICATION NUMBER: US/08/945,567C
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/431,718
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: 08/478,370
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/621,944
; PRIOR FILING DATE: 1996-03-26
; PRIOR APPLICATION NUMBER: PCT/CA96/00264
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1992
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-08-945-567C-3

Query Match 2.2%; Score 161; DB 4; Length 1992;
Best Local Similarity 19.3%; Pred. No. 0.0044;
Matches 241; Conservative 194; Mismatches 494; Indels 320; Gaps 64;

Oy 64 VRPDKCAILKEVYRQIRQIEQCKTISNDDDVQKA---DVSSITGGQIVIDKDSGLPILLQA 120
Db 738 LSPTLPSIDQSSRN---ELGNTIQQDKKSNAAASINDLNTGFMNL--KNNNPNIDPVYS 791
Oy 121 LDGFLFVNEANIVVSE---NVTQLOYKQEDLVNTSVYNIHEDRKDFLK--NLPR 175
Db 792 TYDIVEFANONATTAIVTHTFAKTSKYVY-DVNVDOTIHLTGTDNKKLGVTTKRINK 850
Oy 176 STYNGVSWTNEPOROKSHFNCRM---LMKTPHLLIEDINA--SPMARORYET---MOC 226
Db 851 TSANGTATN-----FNVSDEDALVNAKDIAENLTLAKEIHTTKGTAADTALQT 901
Oy 227 FALSOPRAMEBEDQSCMICVARITTEGRTFPPSNPEFTRHDLSCVAVIDTN--- 283
Db 902 FTVYK-----VDENNNDADD-----ANATVGOQN-ANNQVNTLTLKENGINTIDKNGTV 951
Oy 284 -----SLRSSMRPGFEDIRRCIORFSLNDG-----OSMSQRHYOEAYLVNG 326
Db 952 TEGINTTSLGAKKS-----TLNDGGLSTKNPFGSEIOVGADGVKAKYNNNG 1000
Oy 327 HAETPVRESLADGTIVTAQTSKLEFRNPVYNDRHGFVSTHFLORONGY--RPNPNVYG 384
Db 1001 VVGAGI-----DGT-----TRITREIGFTGT-----NSGLDKSKPHLSK 1035
Oy 385 QGIRPMAAGNSVGVGMSPNGLDMPSSRAYGLADPSTTGOMSGARKGSSNINSLP 444
Db 1036 DGI-----NAGGKKTITNIOGEL---AONSHDAVYGKIYDLKTELEKRISS-7A 1081
Oy 445 GPGMOSPSY-----ONNNYGLNMSSPHGSPGLAPNO-----ONIMISPRNGSPKI 492
Db 1082 KTAONSLHEFSVADBOGNFTV---SNPYSSYTSKTSVYITRAGENGITTKYNNKGVYR 1138
Oy 493 ASHOFSPVAGVHSPMASSGNTGNHSPSSSLALQAISEGVGTSLSTLSSPGPKLDNSP 552
Db 1139 GIDQ---TKGLTTPKLTGVNNGKGIVIDSONCONITIT-GLSWTLANVTNDKG----- 1187

```



```

APPLICATION NUMBER: US/09/421,124
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 23-NOV-1996
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-421-124-16

```

```

Query Match      2.1% Score 158.5; DB 5; Length 2329;
Best Local Similarity 17.6%; Pred. No. 0.0078;
Matches 250; Conservative 195; Mismatches 482; Indels 495; Gaps 59;

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```

QY 7 NLPLASDSRRKLPC-----DTPGQGLTSGEKKRRRQESKYELELLELSAN 55
DB 1052 NLEFDSDSSKNDYVCHHKETDLEFTDQHNICKLSGQ-----PKMEGTQIKED 1102
QY 56 LSDIDMENVKPDCAILKETVROIKEQKTSNDVDYQKADVSTGGVIGDKDSLGP 115
DB 1103 LSDLTFLFV-----AKQOEACHGNTSNKEQLTATKTEQNIKDFETSOT 1145
QY 116 LLLQALDGLFVYNNREANIVFVSENVQYLYQKQEDLVNTSVYNIILHEEDRKDFLKLPLK 175
DB 1146 -FFQTASGKNISAVAKES-----FNKIYVNFQDQPEELHNFSLNSELSDIRKKNMDILSY 1199
QY 176 STVNGVSWTNEPQOKSHFTFCNMLKTPHDLIEDIVASPEMQRVETMGCFLSOPRAM 235
DB 1200 EETDIYK-----HKILKE-----SVF--- 1215
QY 236 MEGBEDLSQCMICVARRITGER--TFPSNPE-----SFTTRHDLGKVVNIIDTNSL 285
DB 1216 -----VGTGNQLVTFQGGPDERDEKIKEPTLLGFTHTASGKKYKIAKESL 1258
QY 286 RSSMRGFEEDIIIRCIORFSLNDGOS-----WSQKRHYQDAYLNGHAETPPVYRFSL 337
DB 1259 -----DKVKNL--FDEKEGQSTSEITSFSHOWAKTLKYREACKD-----LEL 1297
QY 338 ADGTI--VTAOTKSKLPFNPTNDRH-----GFSVTHPIFORQON-----GYR 377
DB 1298 ACETIETTAAPKCKEMONSINNDKNLYSITVPPKILSLNLCROENLTKSKSIFLKV 1357
QY 378 PNDPNVGGGIRPPMAGCNSSVGGMSPNQGLQMPSSRAYGLADPSTT----- 425
DB 1358 VHENVEKETAKSP-ATCYTNQSPSYIENSALAFYITSCSKRTYSQISLLEAKKWLREGI 1416
QY 426 --GQ--MSARVGG-----SSNIAS-----LTPGPKQSPSSSQNNNYGLNMSPP 467
DB 1417 FDOQPERINADYVGNLYENNSSTIAENDKNNLSEKODTYLSNSSMSYSYHSDDEVY 1476
QY 468 HGSPPGLAPNOQIMISPRNGSPKIASHQSPVAGVSHSPASSGNTNHSF-----SS 521
DB 1477 NDSGYLSKNLID-----SGIEPVYLNVEDQNTSFSKVIYSVWKD 1515
QY 522 SLSSALQAISSGVGTSLISTLSSPGPKLIDNSPNNMTTPQSPVSNQDSKSPGLFYCDQNPVE 581
DB 1516 ANAYPQVNEIDICEVELVYTSSSPCKNKNAIKILISN-----SNNEFVGPAFRIASGKI- 1570

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QY 582 SSMQSN-----RDHLDSKESSEVEGAENQRPLESKGHKKLLQTLTCSDDRGHSS 636
DB 1571 --VCVSHETTKKVKNDIFTDSPFSKYK-ENNENKSKICQITIMAGCYEALD-DSEDLIHS 1626
QY 637 LTNSPLDSSCKESSVSVTSPPSGVSSSTSGVSSSTNNHSGSLQEKHRIILKLLQNGNSPA 696
DB 1627 LDN-----DECSHSHKVFAD-----IQSEILQIN--QNNSGLE 1659
QY 697 EVAKITAOATGKDTSSITSCGQGNV-----VKQEOLSPKKEN----- 734
DB 1660 KVSKITSPCDVSLFTSDICKCSIGKILKKSVSANTCGIFSTAGSKSVQVSDASIQNAROYF 1719
QY 735 -----NALLRLLDRDPDALSKELOPQVEGVNKKMSQ-----CTSSITP--SS 777
DB 1720 SELEDSTKQVSKVLEKSNHSDQLTRENTAIRTPEHLISQKGFSYNVNVAFAFGFST 1779
QY 778 SOEKDPKIKTETSESGSDLDNLDAITLGD-----LTSDFYNNSSISSNG 821
DB 1780 ASGQVSLSSLSLHKVKGVEEDPLITERSLHYSPTSRQNVSKILPRVDRKRPHECVNS 1839
QY 822 SHLGTQOVFOGTNSLGLK--SSQSVOSIR-PPYNRAVSLDSPVSVSSPPVKNISAFPM 878
DB 1840 EMEKTSKEFEKLSNINLVEGGSSSENNHSIKVSPY-----LSQFOQ 1879
QY 879 LPKQPMLGCPNRMMDQENCGSSMGP-NNRVYVYOTRPPSSGDMGLPNSKAGRMENPMSN- 936
DB 1880 DKQOLVIGTSLVLEENHVLGKEQASPKNVKMEGKTETSD-----VPVYNTI 1928
QY 937 -----SMGRPGGDVNTSLPRPALGSIPTLPLRSNISGARPVLOQOQMLMRGELPMG 992
DB 1929 EVCSITYKDESENT-----FETEAVALIAAFMEDD-----ELDSKIP-- 1965
QY 993 MGANPYGQAAAQNLGSMWPG--MLSMEOVSHGTONRPLRLNSLDLVGPPS--NLEG 1046
DB 1966 -----SHATSLIFCPENEMEWVLSNRIGK-RRGEPLI-----LVGEPSIKRNL- 2008
QY 1047 QSDERALLDQHLITLSTADTGLLEIDRALGITEPLVNOGALERPQDAFQGOEAAYVMDQ 1106
DB 2009 -----LNEFDRI-----IENQESLAKSKSTPQG-----TIKDR 2037
QY 1107 KAGLYGOTYPAQGPBMGGFHLQGOQSPFSNMNQNQCNFLOGHPRANIMRPRTNT 1166
DB 2038 RLRYH-----HV-----SLEPTICVPRITTKKEQEOINPFTA 2070
QY 1167 PKQLRMQLQRLQGOQFLNOSROALELKMENPTAGAAVNRPMQOQGLFNAQMYAORS 1226
DB 2071 P-----GQFELSKSHLYEHLTEKSSNLAVSGHPFYQ-VSGKNGKM----- 2112
QY 1227 RELI-----SHFRQQRVAMM000000000 1252
DB 2113 RKLITTGRTKPVVPPPEKTSKSHFRVQCVNRINLEGNROKQ 2154

RESULT 11
US-09-421-124-16
Sequence 16, Application US/09421124
GENERAL INFORMATION:
APPLICANT: Futreal, Phillip A
APPLICANT: Wooster, Richard F
APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer
NUMBER OF INVENTION: susceptibility gene and uses thereof.
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CITY: Raleigh
STATE: NC
COUNTRY: USA
ZIP: NC 27622

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,124
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-421-124-16

Query Match 2.1%; Score 158.5; DB 5; Length 2329;
Best Local Similarity 17.6%; Pred. No. 0.0078;
Matches 250; Conservative 195; Mismatches 482; Indels 495; Gaps 59;

QY 7 NDDPLASDSRRKKRLPC-----DPPGGGLGCSGKRRRREGSKYIELAELISAN 55
DB 1052 NLEFPGSSDSKNDYVICIHKDEFDLFTDQHNICLKISGQ-----FMKGGNTQIKED 1102
QY 56 LSDIDNFNKKPKCAILKETVRQIQKEQGTISNDDVDQKADVSTGQYIDKSLGP 115
DB 1103 LSDLFLFLEV-----AKAQCHGNTSNKQLATKTEQNIKQEFESD----- 1145
QY 116 LLLQALDGLFVYVNEANIVFVSENVTOYLOKQEDLVNTSYVNIILHEDRDKFLNLPK 175
DB 1146 -FFQVAGSGNISVAKES-----FNKIVNFFDQKPELHNFSLSNSELHSDIRKNKKDILSY 1199
QY 176 STVNGVSWTNEPQROKSHTFNCRMLKTPHDILEDINASPENKQRYETMQCFALSOGRAM 235
DB 1200 EETDLYK-----HKILKE-----SYP--- 1215
QY 236 MEEGEDLOSMTCVARRITIGER--TFPSNPE-----SEITRHDLSGKVVNIDTNSL 285
DB 1216 -----VGTGNQLVTFOGQPERDEKIKPEPTLIGFTASGKKVKIAXESL 1258
QY 266 RSSMRGPEDITRRCIQRFSLDNGS-----WSQKRHYQEAVALNGHAETPVYRRESL 337
DB 1239 -----DKYKNL-----FDEKEOGTSEITSPSHQWAKTLKRYREACKD-----LEL 1297
QY 338 ADGTI--VTAQTSKLFERNVYTNDRH-----GFVSTHFLQREON-----GYR 377
DB 1298 ACETIEITIAAPKCKEMQNSLNDKMLVSTETVVPKLLSDNLCROTENLTKTSIFLKVK 1357
QY 378 PNPVNVGQIRPPMAGCNSSVSGMSMSPNOGLQMPSSRAYGLADSTT----- 425
DB 1358 VHENVEKEIKASP-ATCYTNQSPYVIEENSALAFYTSGRKTSVSGTSLLEAKKMLREGI 1416
QY 426 --GQ---MSGARYG-----SSNIAS-----LTPGFGMSPSSYONNNGLMMSSPP 467
DB 1417 FDGQPERINTADYVGNVLYEENNSNSTIAENDKNHLSKQDTYLSNMSMSYSYHSDEVY 1476
QY 468 HGSPPLAINGQONIMISPRNRGSPKIASHQFSVYAGVHSHMASSGNTGNHSFS-----SS 521

DB 1477 NDSGLTSKKKLD-----SGLPEVLKAVEQKNTSEKVIASNVKD 1515
QY 522 SLSSALQATSEGVGTSLTSLSSPGPKLDNSPMNMTQPSKYSNODSKSPGLGYCDQNPVE 581
DB 1516 ANAYQTVMEDICVEIELYSSSPCKNNKNAITLSTSN-----SNNEVGPAPFARIASGI- 1570
QY 582 SSMCOSNS-----RDLSDKESKESSEVGAENQRPLESKGHKILLQLLTSCSDDRGHS 636
DB 1571 --VCVSHETIKKVKDIFLTFDSFKVIK-ENNEKSKICQTKIMAGCYEALD-DSEIDLINS 1626
QY 637 LFNPSLDSSCKESSVSVSPSGVSSSTSGCVSTSNMHSGLQEKHRIHLKLONGNPA 696
DB 1627 LDN-----DECSTHSHKVFED-----IQSEELIQHN--QMSGLE 1659
QY 697 EVAKITTAQATGKDTSSITSCGDGNY-----VKQEOLESPKKEN----- 734
DB 1660 KYSKISPCVSLSTSDICKCSIGKILKHSVSNANTGISTAGSKVQVSDASLOANARQVF 1719
QY 735 -----NALLRYLLDRDPSDALSKELQPOVEGVNKKMSQ-----CTSSITP--SS 777
DB 1720 SEIEDSTKQVFESKVLFSKSNHSDQLTREENTAIRPEHLISQKGFSYVNVNSSFSGFST 1779
QY 778 SQEKDPKIKETSESGSGDLNLDLALGD-----LTSDFYNNSSISNG 821
DB 1780 ASGKQVSLIESLHKVKGYLEFEDLIRTEHSLHTYPTSRQNVSKILPRYDKRNPHECVNS 1839
QY 822 SHLGTQKQVFGGNTSLGLK--SSQSVQSIK--PPYNRAVASLSPSVSGSPPKNISAPFM 878
DB 1840 EMKETSCKREFKLSNMLNVEGSGSENNHSIKVSPY-----LSQFQQ 1879
QY 879 LPKQPLGPNPMMDSQENYSGSKGP--NRNVTVQTQTSSCGMGLPNSKAGMEPMNSN- 936
DB 1880 DKQQLVLTGKTVSLVENIHVLGKEQASPKNVKMEIKGTEFFSD-----YVAKTNI 1928
QY 937 ---SMGRPGGDYNTSLPRPALGGSIPTLPLRSNLSIPGARPLYLQOQOQMLQRPPEIMG 992
DB 1929 EVCSTYSKDSERY-----FETEAVEIIRAKAMEDD-----ELTDSKLP-- 1965
QY 993 MGANPYGGAASNOLGSPWDG--MLSMEOVSHGTQNRPLRNSLDDLVGPS--NLEG 1046
DB 1966 -----SHATHSILFTCPENEMEVLNSNRICK-RRGEPLI-----LVGEFSIRKRL-- 2008
QY 1047 QSDERALLDQLHTLLSNDATGLETEDRALGILPELVNGQALEPQODAFQGOEAAVMMQD 1106
DB 2009 -----LNEFDRI-----IENQKSLKASKSPDQ---TIRDR 2037
QY 1107 KAGLVGQFYPAQGPMMQGFHLQGOSSPNSMNMNOGQNPPLQGMHPRANIMRPNT 1166
DB 2038 RLFFVH-----HY-----SLEPTTCVFFPTTKERQETQNPFTA 2070
QY 1167 PQRLRMQLOQRLOGOQFLNQSROALELKNENPTAGAAVMPMOPQOQFLNAQVAAORS 1226
DB 2071 P-----GQEFLSKSHLYEHLTLEKSSMLVAGSHFYQ-VSGNNKNGK----- 2112
QY 1227 RELL-----SHHFROQRYAMMAGQOQOQOQO 1252
DB 2113 RKLITTGPRTKVVPFPFKTSHFHREVCVRNINLEGNRKO 2154

RESULT 12
US-60-248-505-927
; Sequence 927, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 927
LENGTH: 2128
TYPE: PRT
ORGANISM: Human
US-60-248-505-927

Query Match 2.1%; Score 155; DB 6; Length 2128;
Best Local Similarity 17.7%; Pred. No. 0.012;
Matches 195; Conservative 133; Mismatches 419; Indels 352; Gaps 40;

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OY 466 PPHSGPLAP-----NQNMITS 483
DB 457 PPGSGEAPLAGAASLQDEVAEAGRLRLERENRELGLLOVLOGQPGQHLLER 516
OY 484 PR-NRGSPIASHQSPVAVGHP--MASSGNTGNHSSSSLSALQAISEGVSTLST 540
DB 517 PREDPVLPVLEAPQTPVAFDHSQGLVQKARDCGPOALDAPALDVLASAECPQAP 576
OY 541 LSSP-----GPKLDSNNITOPSKVSNDS-KSPLGFTYCOQNPV 580
DB 577 DSDPOAESPLQAAAMPQASDMSPQSSPVETQSPKAGRRSSLQSPASVAPPQPG 636
OY 581 ESSMCSNRDHLSDKESSESV-----EGAENRGPL-----ESKHKKLLQ 623
DB 637 TKIQAPQLLGEGEGREAPQGLVPEAMGLRQGPPEHKQGPSPSSVQLEQCGPNOGLD 696
OY 624 LITCSDDDRGHSS-----LTNSPLDSCKESSSVYTPSGVSSSTSGVSTSNMH 674
DB 697 LATGQAEAREHQRLGRTVPAMQPKPOKSEGLVQWEGPIPESLASGVAEQEALR 756
OY 675 GSLLQEKHI-----LHKLLQNGSPAIVAKITQATCKD----- 710
DB 757 EEVAQLRRRAELGDELEQAARLEAONTAARLSKLAQARRAEAEHREAEQAQMEQA 816
OY 711 ---SSTSCGDGNVVKQEOLEPKKKNALLRLTLDKDDPS-DALSKELOPVEGVNKA 766
DB 817 RLREAVNAG-----QLEESASQREALVEAAGRRERQWRBESRLRAQGEAAEER 869
OY 767 SOCTSTIPSSQEKDKTKTETSEEGSDLDLDAIILDGTTSSDFYNNISSNSHL-- 824
DB 870 ---QVLESEGRHLEAEERERREK-----FALQAELEKAVVRGKELGRLHLQR 916
OY 825 GTRKQVFOGNTSLGLKSSQSVOSIRPPYKRAVSLDSPVSGSPYKKNISAFMLPKQPM 884
DB 917 ELEQAALAEQELREKESQ-----HORYGLEQ----- 944
OY 885 LGSNPRMDSQENYSSGMGNHNTVTQTPSSGDMGLPNSKAGRMEMPMSNSMGRPGD 944
DB 945 -----RLE----- 947
OY 945 YNTSLPRPLGGSIPPLPLRNSNIPGARVYLOOQOQMLQRPGEITPMGMCANFYGOAAS 1004
DB 948 --AELQAAATSKREALEMELKTRA-----LOLEELFQLRQ--PAGLQ---KKRAE 992
OY 1005 NOLGSPQDMLSMEOYSHG--TQNRPLRLNSLDDLVGPPSNLEGQSDERALLDQL---HT 1059
DB 993 POLVETQNRLLLEVERSNMALVAEKALQGLQGLGSLQGRQAEELLQSORAQOES 1052
OY 1060 LLSNTDATILE---EIDRALGIPELVNOGQALEPKQDAFOGQEAIVMMQDQAGLQGY 1115
DB 1053 SRLQAKSVLELQGGELHKKLEV--LEEFYVARAQSEETRGQOQALLDHNK-----QLO 1106
OY 1116 PQAQPPMOC-----GFH--LOGQSFENS-----MNO 1141
DB 1107 RQOEALBEGLVHRHDKANMRALETAHRELQGRHQLQORASVQAQEVLAERERLMD 1166
OY 1142 MNOQGNF-----LOGMHRANIMRPTNPK-----OLRMOL 1174
DB 1167 GHRQKLEELRLQSEHDAQMLLAELSKERELOGERCELRGLARLELERAQLEKOS 1226
OY 1175 QORLQGOQFLNRSQALELKMENPTAGAAVNRPMQPOQGLFMAQVRSRELL----- 1230
```

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DB 1227 QOLRESNQLDLSACRLTQCCELLTOLRSQAE---ENROLLAEVQALSRNELLERSL 1283
OY 1231 ---SHFPROQRV-----AMMQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQ 1280
DB 1284 ESRDHLHREQREYLDQMLRRREKQLYEKIMQYVLEPEGLAQOSPSAPRRRQ 1343
OY 1281 PSM---DGLLAGPTMPQAPQOQFPY---QPNYGMGQOQPPAF--GRVSSPPNMAWSSRMG 1333
DB 1344 SSLCLDETLGAGQRRKL--SRFPVGRSSSESPPGDTPROFRQHRPGLGAFVSHSKGP 1402
OY 1334 -----SONPMQHPQOAS 1346
DB 1403 GVGWENSAETLOEHETDAN 1421
```

```
RESULT 13
US-60-248-505-690
; Sequence 690, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 690
; LENGTH: 884
; TYPE: PRT
; ORGANISM: Human
US-60-248-505-690
```

Query Match 2.1%; Score 151.5; DB 6; Length 884;
Best Local Similarity 19.9%; Pred. No. 0.0061;
Matches 177; Conservative 112; Mismatches 386; Indels 215; Gaps 39;

```
OY 660 SSSTSGGVSTSNMHGSLQEKHR-----LHKLLQNGN----- 693
DB 43 ASDSDNGATLGTRELQLOLQGEFGDFQPCVLHAAVEKNSNLINDSGTISFDEVLATF 102
OY 694 -----SPAEVAKITQATGK--DTSSTSCGDGNVVKQEOLEPKKKNALL 738
DB 103 NLNLICLYDLKSLSELRLQVTRPEKEKLDDVDVQATTBDG---OWTGTSTPOEKRML 158
OY 739 RYLLDRDDPSD-ALSKELOPVEG-----VDKMSQCTSTIPSSQEKDKTK-----T 787
DB 159 -----FSGMASSQLLPBESGAVGNRVDPWRKAKTHNPFGEASEHNDFPKNHLEGD 210
OY 788 ETSEEGSGDLNDLAILGDTTSSDFYNN--ISSNSHLGTRKQVFOGNTSLGLKSSQSV 845
DB 211 EGOGEVADQIQTJEDNEGQKTKPKMAGSKTSSPTERRQGDKEISQEGDEPA--REQS 268
OY 846 QSTRPPYKRAVSLDSPVSGSPYKKNISAFMLPKQPMILGNP-----KMSQENYSS 901
DB 269 SKTRDQFGEQ---EGMLAQSSPP--KEATQRPCEDETQKSTDSKDYCRMFDOE----- 319
OY 902 MGSNNHNTVTQTPSSGDMGLPNSKAGRMEMPMSNSMGRPGDYNTPSLPRALGSGSIPPL 961
DB 320 ---PGKDAQOT-----PATKTNLGER-EDYGRSTSETOEKECTKDL 356
OY 962 PLRNSNIPGARVYLOOQOQMLQRPGEITPMGMCANFYGOAASNOLGSPDMLSMEOYS 1021
DB 357 PVQYGRNS-----ETSDMR-DEKERRRQPEAHGTAQGERBRKW---LVLETQT 403
OY 1022 HGTQNRPL--LRNSLDDLVGPPSNLEGQSDERALLDQLHTLSNTDATILE----- 1070
DB 404 QDKQYLOGLSKSKDAERG--SETQYLSSEGG--DOTHPLELGTAVSDEAEHTKEGTA 459
OY 1071 -----EIDRALGIPELVNOGQALEPKQDAFOGQEAIVM-----MDQKAGLYGOT 1114
```

Db 460 EAFVSKNAAPAEFTLGARE---RTQDLAPLEKQSGVGNTRYTKTHDQPVEEEDQYGE- 515
QY 1115 YPAGCPMPGCFHLOGSPSPNSMM-----NQMNOGNFPLQG-----MHPR----- 1157
Db 516 -DPESPFTQSD---EGSSETPNLSASEGNSSESGELPVGDSQSGDQDQSGHNSVQSGHN 571
QY 1158 -NIMPRNTNTPKOLRMOLQO-----RLQGOQFLNGSRQALELKMNP-TAGGAAYMRPM 1210
Db 572 NNPTQROGTGTEKKRALEAVYPAVRGEDVLTEDQEQPREHKNGCPCTKGGAAYEPNG 631
QY 1211 QPQOGFLNAQVNAQSRRL-----LSHHFROQRYVAMMMQOQOQOQOQOQOQOQOQOQOQO 1265
Db 632 HPEAQESTAGDENRKSLELITGALDEFTQDLSLMLQPGGDSNKLKVGQSPSKERKG 691
QY 1266 QQTQAFSPRPVYATSPMD-----GLLAGPTMPAPQOQFPYQPNYKGOQDPDA- 1315
Db 692 RATEQON-----TLLESDEDENSASLKIQLETKPEPTSEEDSESPQELAGEGGDKSPAK 746
QY 1316 FGAVSSPNAMSSRMGSPQNDPMQHPOA---ASTYQSEKKGWPSGLNARSSPSQOQF 1372
Db 747 KEHNSVWMSLEKOMQDQPCSVGERGAVYSSPLQYLOEKILLOQTNTVTOBEHOKOYQI 806
QY 1373 AHQGNPAVYSM-----VHMGSSGHMGQNMNMPNPGMFPDQ 1412
Db 807 AQASGPCLSVSLTSEISDCSVFFNYQQA--SQPYTRGLPLDESPAGAQE 854

RESULT 14
US-60-248-505-1161
: Sequence 1161, Application US/60248505
: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
: TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
: FILE REFERENCE: C1000918
: CURRENT APPLICATION NUMBER: US/60/248, 505
: CURRENT FILING DATE: 2000-11-15
: NUMBER OF SEQ ID NOS: 1998
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1161
: LENGTH: 1206
: TYPE: PROT
: ORGANISM: Human
: FEATURE:
: NAME/KEY: VARIANT
: LOCATION: (1)...(1206)
: OTHER INFORMATION: Xaa = Any Amino Acid
US-60-248-505-1161

Query Match 2.0%, Score 147.5; DB 6; Length 1206;
Best Local Similarity 17.6%, Pred. No. 0.016;
Matches 241; Conservative 180; Mismatches 468; Indels 481; Gaps 59;

QY 76 VROIQRIEQQKTISSNDQVQKADVSTGQGVYIDKSLPLLQALDGLFVYVREANIV 135
Db 156 VAEKQITEPKKK-EELMKRKRERLARLEGI--ENDQPIILLOSTGL-----VT 203
QY 136 FVSENVATQYLOKQEDLVNTSVYNIHEEDRKDFLKNLPKSTVN-GVSWTNEPQOKSHT 194
Db 204 LLEEDTPRYMASDDP-----HIDPRKPSAITCPMTAAHLSAVFPFGPNSSY-- 251
QY 195 FNCRLMKTPHDLIEDINASEPMR--QRYETMQCFALSQPRAMEEGEDLQSCMTCVARR 252
Db 252 -----LPREIL--NSTKKGRNEEETSDDSLKQTRS-----KYCTETS 289
QY 253 ITTGERTPPSPNESTITTHDLSGKVVNIDTNSLBSMRPGEEDITRKIQRFSLNDQOS 312
Db 290 GVHDSDPYGSQ-----TMDTSLSESKA-----ERLARYAER----- 321
QY 313 WSQRHYQEAVLNGHAETPVYRFLSLADGTIYTAQTKSKLFRNPVTNDRHGVSHTFLQRE 372

Db 322 ---RRQLAEKY--GLTLDP-----ADSEYLSRTYKSR--KEPDAVEKRGKSDKQDESS 369
QY 373 QNGRYRPNPNVQGGIRPMAACNSS---VGMSKSP-----NOGLQMPSSR-AVG 418
Db 370 RDASSLYGTEFTMGLR-TCAGSESKDYALHVGDSDEPVLNLTINQNRQGLSATRQHD 428
QY 419 L--ADPSTQOMGARSRGSSNTASLTPGCMQSPSSYQNNNGLNSSPPHSPGLAP 475
Db 429 LSPAESSSTPFSGR--DSSFTEVPRSPSTPAPPCSRQ-----PPGSPFSDPOLSL 480
QY 476 N-----QONIMISPRNRGSPKIAS-----HOFSPVAVY-----HS-----PMASSG 511
Db 481 EARPVYKREKLIVKESARNSPELASEVYQRRQPAVHVYVQSEHSADRPYPSAAG 540
QY 512 NT-----GNSPSSSSLSALO-----AISEGVTSLL 538
Db 541 STQPIRGYVADPTGHTAKLVTPETPENASECSVAVASATQNVKPPSLVLLEALQSKK 600
QY 539 STLSPGPKLQNSPV-----NMITQPSKYSNQDS---KSP 570
Db 601 TLLALEGGGLVRSPPDPSPRNEDFGKPAVSTVTLQHKELELVNAQPPQAPHQPTERTGSE 660
QY 571 LGFYCDQNPVSESMQSNRDLSPDKSESSVEGAENQRPLESKHKILQLLTCSSD 630
Db 661 MVLTYIQSEPV-----SQDAKPTGHNREASKKRAKVTRELSDFGTGPQDALKYKDPRA 712
QY 631 DRGHSILTNPLDSCCKESSVYVSPGCVSSSTSGCVSSTSNMHGSLLOEKHRLHLKLLQ 690
Db 713 SRRELELPSSTEGPGEISMDFYVS--VAQLRSKAFASANAC-----RRPELKSRYER 765
QY 691 NGNSPAEYAKITQAQATGADTSSITSCGNGNVYKQOLS-----PK 730
Db 766 SAEGGLPTGVERERGSKKPRRYFSPDEKVDERKLSVAAKRLLFREMERKSPDEQVYK 825
QY 731 KKNENAL-----LRYLLDDPSDALSKELQOVGEVDNKKMQCSTSPSSQCKEPKIK 786
Db 826 RRSRTATVEQRLRRQDLSLQPIITTEV-----VIAATIQASAHQK-AKDQ 871
QY 787 T---ETSEGGSGDLNDLAILGDLTSSDFYNNSTISSNGSHLQKQOYFOGTNSLGLKSS 842
Db 872 TNECKELAEQCEPDSTLS-----LAELKALFN-----KLS 902
QY 843 QSVOSIRPPYNR-----AVSLDSPVYSGSSPPYKNISAFMLRQPMPLGCPNPRMD 893
Db 903 QPVSKAISTRRNIDTRQRMNARYQTOPVTLGE--VEQVOSGKLIPSPYAV----- 951
QY 894 SOENYSSMGPPNRNVYTOTPSSGDWGLPNSKAGRMPPMNSNM-GPPGCDYNTSLPRP 952
Db 952 -----NTSVSTYAST-----VAPMTAGDLRTKRPPLDHNASATDY 985
QY 953 ALGGSIPPLPLRSNSIPGARVYLQOQOQMLQMRPELIPMGANGPNYGOAASNOLGSMPD 1012
Db 986 KFSSSI-----ENDSPVSRILKSQ-----AM-- 1007
QY 1013 GMLSMEQVSHGTQNRPLR-----NSLDDVYGPNSLEGQSDERALLDQLTLLSNIDAT 1067
Db 1008 -----QPLVEESSENGMLREYGETESKRALTGROSGMEKYG----- 1043
QY 1068 GLEIEDRALGIPELVNOQALPEKODAFQGOEAMVMMQKAGLYGQYPAQG-----PP 1121
Db 1044 SFEAEASYPLLNRRREG-----DSHKESKYAV-----PRGSGLERANPP 1093
QY 1122 MQGGFHLQGSFSPNSMMQNNQGNFPLQGMHPRANIMPRRTYTPKQLRMQLOORLQGO 1181
Db 1084 IT---HLGDEPKRFS--WAKMNAQCNLDLRD-----RLPFEKYEVE 1120
QY 1182 QFLNDSKQALELKMENPTAGGAAYVRPMQOQFLNAQVNAQSRRELSHHFPOQRYAM 1241
Db 1121 NYMKRKFELRAAEFGPEPTS-----EOTGTAAGKTIYAQTAVP----- 1157
QY 1242 MMQO 1291
Db 1158 -----SWKQDSDSEQPOEKLCNPKCAMFA--AGEIKTPTGGBLSDSPS 1198

RESULT 15
US-60-248-505-714
Sequence 714, Application US/60248505
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
FILE REFERENCE: C1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 714
LENGTH: 2000
TYPE: PRT
ORGANISM: Human
US-60-248-505-714

Query Match 2.08; Score 147; DB 6; Length 2000;
Best local similarity 18.5%; Pred. No. 0.034;
Matches 168; Conservative 130; Mismatches 342; Indels 268; Gaps 35;

QY 425 TGQMSGARYGSSNIA-SLTGPGKQSP-----SSY-----QNNNYG----- 460
DB 3 SSRSGIYVGEOSTYVQDSATPSPPPPQPTERTPTSAIYRLRQVSYPTAECCOHGI 62
QY 461 LNMSSPPHGS--PGLAPNOQIMISPRNRGPKTIASHQFSPVAGVHSPMASSGNTGNHSF 518
DB 63 LCICSRGCGTVPFLPQHDVPPASARATTPSSSFVOTEP---FHPEQASSTQOQDGL 119
QY 519 SS--SSLSALQAISEG---VGTSLSTLSLSPGPKLDNSPNNNITO--PSKVSNDPSPL 571
DB 120 LNRPSAFSTVQSTAGNTLRNLSLGPTRRLSGPLSHPSRYHREIAPGLGSEWTRIVL 179
QY 572 GFYCDQNVESMCOQSNRDLSDKESKESVEGAEENORGPLESKGHKLQQL----- 625
DB 180 SL-----NSRSE-----AESMPPTSAVSLSLVLRQDECG 212
QY 626 -----TSSSDRGHSITNSPLDSSCKESSVSPGVSSTSGVSTSNMHSLLQ 679
DB 213 SQASVYTATGCRGPPA-----SGLATESDGGNGSSONNSGSTRH 252
QY 680 E-----KHRLHKLQ--NGNSPAEYAKITAOATGKDTSSITSCGDGNNYKQEQ 727
DB 253 ELQCDLRFLELDRLQELDQSLGEPQ-----TQQAQEMLNNNIESPPSH---QP 302
QY 728 SPKKENNAL-----RYLLDRDPSDALSKELQPOVEGVNKKMSOCTSS--TI 774
DB 303 TPHSSENNNSLRGLNRCRACHNLTFTNNDTLRWERTTPNYSGEASSSQVPPSSFESEV 362
QY 775 PSSSOEKDPKIKTETSESGDLDLMDALIGDLTSSDFYNNIS--SNGSHLGTRQOVPFG 833
DB 363 PSSGSQPLPLERTGQTPSSSRL-----ELSSDOEERTVGAFNOETGHEMERITQ 414
QY 834 TNSLGLKSSQGVQSIIRPPYR--AVSLDSPVYSGSSPPVKNISAFPMIPKOPMLGNPR 890
DB 415 SSRSGTVQSEALHODMPESSEEDSLRLSPAAYYAQRMIOYLSRDSIRQSMRYQQNR 474
QY 891 MMDQENYGSMSGPNRNVITYQTTPSSGDWGLPNSKAGRMEMPNSNSMGPRGGDYNTSLP 950
DB 475 LRSSTSSSSSDNOGSPVGTDLFEDEFDNG-----DRSRHAPRNARMS 519
QY 951 RPALGGSIFTLPLRSNSIPGARPLYLOOQOQMLQMRPEIPMGMGANPYGQAASNQLGSM 1010
DB 520 APSLGRFPYPRFLPEYLYPA-GIHERGQ-----PG----- 550
QY 1011 PDGMLSMQVSHGTQNRPLLRNSLDDLVPSPSNEGQSDERALDQDLTLTSLNTDQGLE 1070
DB 551 -----LATHSSVNRVLGAVIGD-----GQS-----AVNIANTLYLQMMDFTKFD 589

QY 1071 EIDRALGIPELVNOGQALEPKQDAFQGOEAAV--MMDQKAGLY-----GOTYPAQG 1119
DB 590 -----LPEISN-----ASVNYLVQCKIKYINDASCDISADGQLLAIFI 626
QY 1120 PPMQGFHLOGQSPSPF-----NSMNNOMNOQGNFPLQGMHPRANIMR 1161
DB 627 PSSQKGFDEGLAVYSLAPHNLGEMLYTKRFPNAISVLSLPMGRYVMVGLASRRILLH 686
QY 1162 PRTNTPKQLRMQLOGQOQFLNQSROALEIKMENPTAGGAA-----VMRPMQ-P 1212
DB 687 PSTEHMVAQVFRLOQAHGGETSMREGVAVAKKDVIHMPKHELADKNDVNLHVKKAMQSLK 746
QY 1213 QQGFLNAQ 1220
DB 747 SRGIYKEQ 754

Search completed: April 19, 2001, 16:54:07
Job time: 491 sec

OY 64 SLQEKHRIHLKLLQNGSPAEVAKITQAOTGKDTSSITSCGDNVVKQOLSPKKENN 123
Db 67 S-----SSSSDSESEAFETKREESKSSSSSSSSSSDSEEBEKEETKKEES 113

RESULT 2
US-08-320-559-30
; Sequence 30, Application US/08320559
; Patent No. 5631135
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Cnaan, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
; TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
; TITLE OF INVENTION: All-1 Region
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5631135rls
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,559
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/062,443
; FILING DATE: 14 MAY 1993
; PRIOR APPLICATION DATA: US/07/971,094
; APPLICATION NUMBER: 30-OCT-92
; FILING DATE: 30-OCT-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/888,830
; FILING DATE: 27-MAY-92
; PRIOR APPLICATION DATA: US/07/805,093
; APPLICATION NUMBER: 11-DEC-91
; FILING DATE: 11-DEC-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0855
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-320-559-30

Query Match 11.78; Score 82; DB 1; Length 568;
Best Local Similarity 24.78; Pred. No. 1;
Matches 42; Conservative 20; Mismatches 56; Indels 52; Gaps 5;
OY 7 KLLQL-----LTCSSDRGSHSLTNSPLDSCCKESSVSPSGVSSSTGCVST- 58
Db 133 KLLKAGGDPNRSHITSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSTS 192
OY 59 -----SNMHSILQEKHRIHLKLLQNG-----NSPAEVAKITQAOT 94
Db 193 FSKPRHKLMEKREKPSKDSREHKSAPFKERPRDHNKSSKESKPKREKPLKEKIVPKMA 252

OY 95 GKDT-----SITSCGDN-----VVKQOLSPKKENNA 124
Db 253 FKPEKPSKREKPPDSNLTITSGDDKKAPSKRPPISSSELSAKKRRKS 302

RESULT 3
US-08-545-860D-30
; Sequence 30, Application US/08545860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Cnaan, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; STREET: No. 6040140rls
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,860D
; FILING DATE: 07-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE: 22-APR-1994
; PRIOR APPLICATION DATA: PCT/US92/10930
; APPLICATION NUMBER: 09-DEC-1992
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/327,392
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/320,559
; FILING DATE: 11-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,443
; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA: US 07/971,094
; APPLICATION NUMBER: 30-OCT-1992
; FILING DATE: 30-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,839
; FILING DATE: 27-MAY-1992
; PRIOR APPLICATION DATA: US 07/805,093
; APPLICATION NUMBER: 11-DEC-1991
; FILING DATE: 11-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-860D-30

Query Match	10.7%;	Score 75;	DB 1;	Length 212;
Best Local Similarity	20.6%;	Pred. NO. 1.4;		
Matches 29;	Conservative 25;	Mismatches 49;	Indels 38;	Gaps 4;

[illegible]

RESULT 14
US-09-046-894-35
; Sequence 35, Application US/09046894
; Patent No. 6100857

GENERAL INFORMATION: David
APPLICANT: Ralph, David
APPLICANT: An, Gang
APPLICANT: O'Hara, Mark S.
APPLICANT: Veltiel, Robert
TITLE OF INVENTION: DIAGNOSIS OF DISEASE STATE USING mRNA
PROFILES IN PERIPHERAL LEUKOCYTES
TITLE OF INVENTION: PROFILES IN PERIPHERAL LEUKOCYTES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; C:\IBMPC\BATCH\IBMPATENTIN.BAT
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? FILING DATE: Concurrently Herewith
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 60/041,576
? FILING DATE: 24-MAR-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Nakashima, Richard A.
? REGISTRATION NUMBER: P-42,023
? REFERENCE/DOCKET NUMBER: UROC:014
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312) 418-3000
? TELEFAX: (312) 474-7577
? INFORMATION FOR SEQ ID NO: 35:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 761 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: linear
US-09-046-894-35

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Query Match 10.6%; Score 74.5; DB 4; Length 761;
Best Local Similarity 27.3%; Pred. No. 9.9;
Matches 36; Conservative 17; Mismatches 42; Indels 37; Gaps 5.

OY 14 TCSSD-----RGHSLLNSPLDSCKRESSVTSFSGVSSSTGCGVSTSNMHGSL 66
||||| :||: ||| :||: ||| :||: ||| :||: ||| :||: ||| :||: |||
599 TCCSDALGPMSTRDHGLASISPSRSPGHADFLTP--LSPTASQG--SFSFCVGSLTE 654

QY	67	QEK -HRIHLKLONGNSPAEYAKITTAOTGDTSSITSCGDGNVVKOEOLSPKKKENAL	125
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QY	126	LRYLLDRDPSD	137
	:::::		:::
Db	690	PAPAVSDGESD	701

RESULT 15
US-08-933-750C-45
; Sequence 45, Application US/08933750C
; Patent No. 5932442

GENERAL INFORMATION:
 APPLICANT: Lal, Preeti
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Bandman, Olga
 APPLICANT: Shah, Purvi
 APPLICANT: Au-Young, Janice
 APPLICANT: Yue, Henry
 APPLICANT: Guegler, Karl J.
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
 NUMBER OF SEQUENCES: 98
 CORRESPONDENCE ADDRESS:

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1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Diskette
3 COMPUTER: IBM Compatible
4 OPERATING SYSTEM: DOS
5 SOFTWARE: FASTSEQ for Windows Version 2.0.
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/933,750C
8 FILING DATE: September 23, 1997

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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US

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: INFORMATION FOR SEQ ID NO: 45
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 811 amino acids
:
: type: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
:
: LIBRARY: L1970T04
:
: CLONE: 2515476
:
: US-08-933-750C-45

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	Query Match	Similarity	27.6%, Best Local	Score 74.5, Local Similarity 36;	DB 2; Conservative	Length 811; Pred. No. 11; Matches	Mismatches 42;	Indels 37;	Gaps 5;
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Dd	649	TCCSSALGPSTTEHGSLSTSPUSRSFGSHDFLLTP--LSPTAQG--SPSFVCVSLE	704		: : : :	:	:	:	:
ZY	67	OEK-HRILHKLQNQNSPAEYAKITTAQTAGKTSSITSCGDENVVKOEQLSPKKRENNAI	125		: : : :	:	:	:	:

Db	705	EDSPFPSEFAQMLRGKAKADVMPXTA-----		PKDENSLV 739
Qy	126	LRYLDRDRDPSD 137		
Db	740	PPAPVDSGSED 751		

Search completed: April 19, 2001, 16:50:51
Job time: 299 sec

GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2001, 16:54:00 ; Search time 147.68 Seconds
(without alignments)
152.489 Million cell updates/sec

Title: US-09-041-994-2_COPY_613_752

Perfect score: 703

Sequence: 1 LESKGHKKLLQLTCSDDR.....ENNALLRYLLDRDPDSALSL 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1009251 seqs, 160854530 residues

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	703	100.0	1415	19	US-09-513-066-2
3	700	99.6	951	15	US-09-125-635-8
4	700	99.6	1420	15	US-09-125-635-8
5	628.5	89.4	1398	19	US-09-513-066-14
6	628.5	89.4	1402	15	US-09-125-635-12
7	628.5	89.4	1402	18	US-09-445-353A-2
8	540	76.8	149	23	US-60-236-359-19468
9	482	68.6	1391	19	US-09-513-066-15
10	292.5	41.6	1127	23	US-60-258-273-113

11	292.5	41.6	1464	12	US-08-891-640-2	Sequence 2, Appli
12	287.5	40.9	151	23	US-60-182-918-63	Sequence 63, Appli
13	286.5	40.8	1462	18	US-09-445-353A-3	Sequence 3, Appli
14	192.5	27.4	193	23	US-60-177-667-86	Sequence 86, Appli
15	192.5	27.4	193	23	US-60-177-667-87	Sequence 87, Appli
16	188.5	26.8	48	12	US-08-891-640-5	Sequence 5, Appli
17	186.5	26.5	1036	12	US-08-891-640-3	Sequence 3, Appli
18	186.5	26.5	1061	11	US-08-701-154A-5	Sequence 5, Appli
19	181	25.7	75	23	US-60-196-714-529	Sequence 529, App
20	172	24.5	34	16	US-09-281-717-15	Sequence 15, Appli
21	172	24.5	34	16	US-09-281-717-18	Sequence 18, Appli
22	168	23.9	34	16	US-09-281-717-21	Sequence 21, Appli
23	141	20.1	27	1	PCT-US99-24956-5	Sequence 5, Appli
24	141	20.1	27	1	PCT-US99-24956-5	Sequence 5, Appli
25	141	20.1	27	1	PCT-US99-30947-5	Sequence 19, Appli
26	141	20.1	32	16	US-09-281-717-19	Sequence 22, Appli
27	141	20.1	32	16	US-09-281-717-22	Sequence 17, Appli
28	139	19.8	34	16	US-09-281-717-17	Sequence 14, Appli
29	135	19.2	34	16	US-09-281-717-14	Sequence 20, Appli
30	135	19.2	34	16	US-09-281-717-20	Sequence 16, Appli
31	134	19.1	32	16	US-09-281-717-16	Sequence 2, Appli
32	128	18.2	25	1	PCT-US99-24956-2	Sequence 2, Appli
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35	128	18.2	25	19	US-09-513-066-26	Sequence 26, Appli
36	106	15.1	34	16	US-09-281-717-9	Sequence 9, Appli
37	105	14.9	34	16	US-09-281-717-6	Sequence 6, Appli
38	105	14.9	34	16	US-09-281-717-12	Sequence 12, Appli
39	97	13.8	491	15	US-09-107-532-6115	Sequence 6115, Ap
40	97	13.8	1113	20	US-09-618-425-9	Sequence 9, Appli
41	95	13.5	18	19	US-09-513-066-24	Sequence 24, Appli
42	93.5	13.3	25	1	PCT-US99-24956-3	Sequence 3, Appli
43	93.5	13.3	25	1	PCT-US99-24956-3	Sequence 3, Appli
44	93.5	13.3	25	1	PCT-US99-30947-3	Sequence 3, Appli
45	93.5	13.3	1357	23	US-60-173-464-29513	Sequence 29513, A

ALIGNMENTS

RESULT 1
US-09-041-994-2
; Sequence 2, Application US/09041994
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; APPLICANT: Li, Hui
; TITLE OF INVENTION: Transcriptional Coactivator for Nuclear
; TITLE OF INVENTION: Hormone Receptors
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive and Cockfield
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,994
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Liepmann, W. Hugo
; REGISTRATION NUMBER: 20,407
; REFERENCE/DOCKET NUMBER: UMW-026-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-227-7400
; TELEFAX: 617-742-4214
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-041-994-2

Query Match          100.0%; Score 703; DB 14; Length 1415;
Best Local Similarity 100.0%; Pred. No. 7.8e-60;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESKGHKLLQLLTCSSDDRGHSSLTNSPLDSSCKESSVSVTSPSGVSSSTSGVSSTSN 60
    |||||||
Db 613 LESKGHKLLQLLTCSSDDRGHSSLTNSPLDSSCKESSVSVTSPSGVSSSTSGVSSTSN 672

QY 61 MHGSLLOEKHRIHLKLLQNGNSPAEVAKITAQATGKDTSSITSCGNGNVYKQQLSPKKK 120
    |||||||
Db 673 MHGSLLOEKHRIHLKLLQNGNSPAEVAKITAQATGKDTSSITSCGNGNVYKQQLSPKKK 732

QY 121 ENNALLRYLLDRDDPSDALS 140
    |||||||
Db 733 ENNALLRYLLDRDDPSDALS 752

RESULT 2
US-09-513-066-2
; Sequence 2, Application US/09513066
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; APPLICANT: Leo, Christopher
; APPLICANT: Li, Hui
; TITLE OF INVENTION: NOVEL USES FOR THE RAC3 TRANSCRIPTIONAL COACTIVATOR OF
; FILE REFERENCE: UMG-026CP
; CURRENT APPLICATION NUMBER: US/09/513,066
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: USSN 09/041,994
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: USSN 60/073,674
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-066-2

Query Match          100.0%; Score 703; DB 19; Length 1415;
Best Local Similarity 100.0%; Pred. No. 7.8e-60;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESKGHKLLQLLTCSSDDRGHSSLTNSPLDSSCKESSVSVTSPSGVSSSTSGVSSTSN 60
    |||||||
Db 613 LESKGHKLLQLLTCSSDDRGHSSLTNSPLDSSCKESSVSVTSPSGVSSSTSGVSSTSN 672

QY 61 MHGSLLOEKHRIHLKLLQNGNSPAEVAKITAQATGKDTSSITSCGNGNVYKQQLSPKKK 120
    |||||||
Db 673 MHGSLLOEKHRIHLKLLQNGNSPAEVAKITAQATGKDTSSITSCGNGNVYKQQLSPKKK 732

QY 121 ENNALLRYLLDRDDPSDALS 140
    |||||||
Db 733 ENNALLRYLLDRDDPSDALS 752

RESULT 3
US-09-125-635-8
; Sequence 8, Application US/09125635
; GENERAL INFORMATION:
; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
```

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; FILE REFERENCE: 49944
; CURRENT APPLICATION NUMBER: US/09/125,635
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-125-635-8

Query Match          99.6%; Score 700; DB 15; Length 951;
Best Local Similarity 99.3%; Pred. No. 8.8e-60;
Matches 139; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESKGHKLLQLLTCSSDDRGHSSLTNSPLDSSCKESSVSVTSPSGVSSSTSGVSSTSN 60
    |||||||
Db 314 LESKGHKLLQLLTCSSDDRGHSSLTNSPLDSSCKESSVSVTSPSGVSSSTSGVSSTSN 373

QY 61 MHGSLLOEKHRIHLKLLQNGNSPAEVAKITAQATGKDTSSITSCGNGNVYKQQLSPKKK 120
    |||||||
Db 374 MHGSLLOEKHRIHLKLLQNGNSPAEVAKITAQATGKDTSSITSCGNGNVYKQQLSPKKK 433

QY 121 ENNALLRYLLDRDDPSDALS 140
    |||||||
Db 434 ENNALLRYLLDRDDPSDALS 453

RESULT 4
US-09-125-635-4
; Sequence 4, Application US/09125635
; GENERAL INFORMATION:
; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
; FILE REFERENCE: 49944
; CURRENT APPLICATION NUMBER: US/09/125,635
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-125-635-4

Query Match          99.6%; Score 700; DB 15; Length 1420;
Best Local Similarity 99.3%; Pred. No. 1.5e-59;
Matches 139; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESKGHKLLQLLTCSSDDRGHSSLTNSPLDSSCKESSVSVTSPSGVSSSTSGVSSTSN 60
    |||||||
Db 613 LESKGHKLLQLLTCSSDDRGHSSLTNSPLDSSCKESSVSVTSPSGVSSSTSGVSSTSN 672

QY 61 MHGSLLOEKHRIHLKLLQNGNSPAEVAKITAQATGKDTSSITSCGNGNVYKQQLSPKKK 120
    |||||||
Db 673 MHGSLLOEKHRIHLKLLQNGNSPAEVAKITAQATGKDTSSITSCGNGNVYKQQLSPKKK 732

QY 121 ENNALLRYLLDRDDPSDALS 140
    |||||||
Db 733 ENNALLRYLLDRDDPSDALS 752

RESULT 5
US-09-513-066-14
; Sequence 14, Application US/09513066
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
```

APPLICANT: Leo, Christopher
APPLICANT: Li, Hui
TITLE OF INVENTION: NOVEL USES FOR THE RAC3 TRANSCRIPTIONAL COACTIVATOR OF
STERIOD NUCLEAR RECEPTORS
FILE REFERENCE: UMG-026CP
CURRENT APPLICATION NUMBER: US/09/513,066
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: USSN 09/041,994
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: USSN 60/073,674
PRIOR FILING DATE: 1998-02-04
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 1398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-066-14

Query Match 89.4%; Score 628.5; DB 19; Length 1398;
Best Local Similarity 89.3%; Pred. No. 1.6e-52;
Matches 125; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
QY 1 LESKGHKKLLQLLTCCSDDRGHSSLTNSPLDSSCKESSVSVTSPSGVSSSTSGVSSSTSN 60
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Db 606 LESKGHKKLLQLLTCCSDDRGHSSLTNSPLDPCNCKDSSVSVTSPSGVSSSTSGVSSSTSN 665
QY 61 MHGSLLOEKHRLHLKLLONGNSPAEVAKITAGATGKDTSSITSCDGNVNVKQEQLSPPKK 120
|||||
Db 666 VHGSLLQEKHRLHLKLLONGNSPAEVAKITAEATGKDTSSITASCCEG-TTROEQLSPPKK 724
QY 121 ENNALLRYLLDRDPDSALS 140
|||||
Db 725 ENNALLRYLLDRDPDSVLA 744

RESULT 6
US-09-125-635-12
Sequence 12, Application US/09125635
GENERAL INFORMATION:
APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
FILE REFERENCE: 49944
CURRENT APPLICATION NUMBER: US/09/125,635
CURRENT FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: 60/049,728
PRIOR FILING DATE: 1997-06-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 1402
TYPE: PRT
ORGANISM: Mus musculus
US-09-125-635-12

Query Match 89.4%; Score 628.5; DB 15; Length 1402;
Best Local Similarity 89.3%; Pred. No. 1.6e-52;
Matches 125; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
QY 1 LESKGHKKLLQLLTCCSDDRGHSSLTNSPLDSSCKESSVSVTSPSGVSSSTSGVSSSTSN 60
|||||
Db 605 LESKGHKKLLQLLTCCSDDRGHSSLTNSPLDPCNCKDSSVSVTSPSGVSSSTSGVSSSTSN 664
QY 61 MHGSLLOEKHRLHLKLLONGNSPAEVAKITAGATGKDTSSITSCDGNVNVKQEQLSPPKK 120
|||||
Db 665 VHGSLLQEKHRLHLKLLONGNSPAEVAKITAEATGKDTSSITASCCEG-TTROEQLSPPKK 723
QY 121 ENNALLRYLLDRDPDSALS 140
|||||
Db 724 ENNALLRYLLDRDPDSVLA 743

RESULT 7
US-09-445-353A-2
Sequence 2, Application US/09445353A
GENERAL INFORMATION:
APPLICANT: Rosenfeld, et al., Michael
TITLE OF INVENTION: A Transcription Factor Coactivator Protein, p/CIP
FILE REFERENCE: 6627-PAL021
CURRENT APPLICATION NUMBER: US/09/445,353A
CURRENT FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1402
TYPE: PRT
ORGANISM: Mus musculus
US-09-445-353A-2

Query Match 89.4%; Score 628.5; DB 18; Length 1402;
Best Local Similarity 89.3%; Pred. No. 1.6e-52;
Matches 125; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
QY 1 LESKGHKKLLQLLTCCSDDRGHSSLTNSPLDSSCKESSVSVTSPSGVSSSTSGVSSSTSN 60
|||||
Db 606 LESKGHKKLLQLLTCCSDDRGHSSLTNSPLDPCNCKDSSVSVTSPSGVSSSTSGVSSSTSN 665
QY 61 MHGSLLOEKHRLHLKLLONGNSPAEVAKITAGATGKDTSSITSCDGNVNVKQEQLSPPKK 120
|||||
Db 666 VHGSLLQEKHRLHLKLLONGNSPAEVAKITAEATGKDTSSITASCCEG-TTROEQLSPPKK 724
QY 121 ENNALLRYLLDRDPDSALS 140
|||||
Db 725 ENNALLRYLLDRDPDSVLA 744

RESULT 8
US-60-236-359-19468
Sequence 19468, Application US/60236359
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
FILE REFERENCE: MdhMORF-4P
CURRENT APPLICATION NUMBER: US/60/236,359
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 21709
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 19468
LENGTH: 149
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL034418.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
OTHER INFORMATION: EST_HUMAN HIT: AW503706.1, EVALUE 9.00e-51
OTHER INFORMATION: SWISSPROT HIT: Q58434, EVALUE 5.30e-01
US-60-236-359-19468

RESULT 11
US-08-891-640-2
; Sequence 2, Application US/08891640
; GENERAL INFORMATION:
; APPLICANT: Chambon, Pierre
; APPLICANT: Gronemeyer, Hinrich
; APPLICANT: Voegel, Johannes
; APPLICANT: Lutz, Yves
; TITLE OF INVENTION: Transcriptional Intermediary Factor-2
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600

[illegible]

Qy 63 GSLQEKHRIILHKLLQNGNSPAEVAKITAQATGKDTSSITSGDGNV-----VKQQLSP 117
Db 70 SS-LTERHKILRLQEG-SPSDITTLSEPPKKDSASTSVYTGQYQGNSSIKLELDAS 127
Qy 118 KKE--NNALLRYLLDRDD 134
Db 128 KKEKXDHQLRYLLDKDE 146

Search completed: April 19, 2001, 16:54:03
Job time: 490 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2001, 16:54:07 ; Search time 7.55 Seconds
(without alignments)
46.942 Million cell updates/sec

Title: US-09-041-994-2_COPY_613_752

Perfect score: 703
Sequence: 1 LESKGHKKLLQLLTCCSDR.....ENNALLRYLLDRDDPSDALS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 12259 seqs, 2531507 residues

Total number of hits satisfying chosen parameters: 12259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	11.1	1589	5	US-09-421-124-189
2	78	11.1	1589	5	US-09-421-124-189
3	70.5	10.0	826	5	US-09-533-077-330
4	70	10.0	509	5	US-09-739-449-11239
5	66.5	9.5	296	5	US-09-739-449-9535
6	65	9.2	382	5	US-09-739-449-8471
7	65	9.2	787	5	US-09-739-449-9028
8	63.5	9.0	2000	6	US-60-248-505-714
9	63	9.0	775	5	US-09-739-449-10931
10	63	9.0	1833	4	US-08-945-567C-4
11	63	9.0	1992	4	US-08-945-567C-3
12	63	9.0	2329	5	US-09-421-124-16
13	63	9.0	2329	5	US-09-421-124-16
14	63	9.0	3418	5	US-09-421-124-44
15	63	9.0	3418	5	US-09-421-124-44
16	62.5	8.9	353	5	US-09-292-858B-23
17	62.5	8.9	539	5	US-09-533-077-326
18	62	8.8	751	5	US-09-739-449-9898
19	61	8.7	373	5	US-09-819-142-2
20	61	8.7	516	5	US-09-739-449-13067
21	61	8.7	902	6	US-60-248-505-973
22	61	8.7	992	6	US-60-248-505-1112
23	60.5	8.6	580	6	US-60-248-505-1300
24	60.5	8.6	661	6	US-60-248-505-739
25	60.5	8.6	1731	6	US-09-739-449-8331
26	59.5	8.5	152	1	PCT-US01-01350-146
27	59.5	8.5	213	5	US-09-739-449-11798

28	59.5	8.5	315	6	US-60-277-380-40	Sequence 40, App1
29	59.5	8.5	414	5	US-09-739-449-11691	Sequence 11691, A
30	59.5	8.5	934	6	US-60-248-505-1027	Sequence 1027, Ap
31	59.5	8.5	933	5	US-09-207-359B-8	Sequence 8, App1
32	59	8.4	198	5	US-09-739-449-10949	Sequence 10949, A
33	59	8.4	537	6	US-60-248-505-1227	Sequence 1227, Ap
34	59	8.4	4563	5	US-09-802-640-32	Sequence 32, App1
35	58.5	8.3	269	5	US-09-792-024-114	Sequence 114, App1
36	58.5	8.3	284	6	US-60-248-505-906	Sequence 906, App
37	58.5	8.3	352	5	US-09-514-450-5	Sequence 5, App1
38	58.5	8.3	587	6	US-60-248-505-742	Sequence 742, App
39	58.5	8.3	646	6	US-60-248-505-935	Sequence 935, App
40	58	8.3	310	5	US-09-739-449-10889	Sequence 10889, A
41	58	8.3	343	5	US-09-739-449-9832	Sequence 9832, Ap
42	57.5	8.2	608	5	US-09-739-449-10801	Sequence 10801, A
43	57.5	8.2	715	5	US-09-792-024-85	Sequence 85, App1
44	57	8.1	274	5	US-09-813-408-17	Sequence 17, App1
45	57	8.1	508	5	US-09-563-997-4	Sequence 4, App1

ALIGNMENTS

RESULT 1
US-09-421-124-189
Sequence 189, Application US/09421124
GENERAL INFORMATION:
APPLICANT: Futreal, Phillip A
APPLICANT: Ashworth, Richard F
APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESS: Bell Seltzer Park & Gibson
STREET: 310 USB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CITY: Raleigh
STATE: NC
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421.124
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/755.587
FILING DATE: 25-NOV-1996
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 1589 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-421-124-189
Query Match 11.1%, Score 78, DB 5, Length 1589;

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Best Local Similarity 24.1%; Pred. No.1.9;
Matches 40; Conservative 20; Mismatches 62; Indels 44; Gaps 6

OY 2 ESKGKKLLQLLTGSSDDRGHSSL--TNSPLDSCKESSVSVTSPGVSSSTSGGVSSSTS 59
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1319 EMDGAKOQLSSVLEGNKPHHSVRENSVSVSTGCVLSLPKPLPGNNVSVSFGSTAG 1378
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 60 NMHSSLGDEKHRIHLKL-----LQNGNSPAEYAKI----- 89
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1379 ---GLVTVYESALHKVGMLEFPDLIRTEHTLQHSPIPEDVSKLIPQCAEIRTPPEYV 1435
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 90 -TAQATGKDTSSI-----TSCGDGNVVKOE---QLSPKKENNALI 126
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1436 NSLQATYNDKSSLPSPNYKSSSGSGNTQSIENVSLQLSQMRNDQTQL 1481
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
US-09-421-124-189
: Sequence 189. Application US/09421124
: GENERAL INFORMATION:
: APPLICANT: Futreal, Phillip A
: APPLICANT: Wooster, Richard F
: APPLICANT: Ashworth, Alan
: APPLICANT: Stratton, Michael R
: TITLE OF INVENTION: Materials and methods relating to the
: TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer
: TITLE OF INVENTION: susceptibility gene and uses thereof.
: NUMBER OF SEQUENCES: 222
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Bell Seltzer Park & Gidson
: STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
: CITY: Raleigh
: STATE: NC
: COUNTRY: USA
: ZIP: NC 27622
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EP0)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/421.124
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/755.587
: FILING DATE: 25-NOV-1996
: APPLICATION NUMBER: GB 9523959.6
: FILING DATE: 23-NOV-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9525555.0
: FILING DATE: 14-DEC-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9617961.9
: FILING DATE: 28-AUG-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Kenneth D Sibley
: REGISTRATION NUMBER: 31,665
: REFERENCE/DOCKET NUMBER: 5405-135
: INFORMATION FOR SEQ ID NO: 189:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1589 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-09-421-124-189

Query Match 11.1%; Score 78; DB 5; Length 1589;
Best Local Similarity 24.1%; Pred. No.1.9;
Matches 40; Conservative 20; Mismatches 62; Indels 44; Gaps 6;

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Oy 60 NMHSGHLEKRIHLKL-----LONGNSPAEVAKI----- 89
Db 1379 ---GLVTVSESAHLKVGCMLEFPDLITEHTLQHSPIPEDVSKILLPQPCAIRPEYV 1435
Oy 90 -TAQATGKDTSSI-----TSCGDGNVVKOE---QLSPKKENMALL 126
Db 1436 NSLQKTYNDKSSLPENYKESGSSGNTQSTIEVSLQLSQMERNDPTQL 1481

RESULT 3
; Sequence 330, Application US/09533077
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C5
; CURRENT APPLICATION NUMBER: US/09/533.077
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 800
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-077--330

Query Match 10.0%; Score 70.5; DB 5; Length 826;
Best Local Similarity 26.4%; Pred. No. 4.6;
Matches 28; Conservative 19; Mismatches 44; Indels 15; Gaps 4;

Oy 28 SPLDSS-----CKESSVYVTPSGVSSSTPSGVSSTSNMHGSLLOEKRIHL-KLLQN 79
Db 581 SPLESSASPEASASPOSTVTFEQFOIODEPTANATTATTATDELKTVKRDMEDIKILIA 640
Oy 80 GNSPAEVAKITAAQATG---KDTSSITS---CGGGSNVKQQLSPK 118
Db 641 SPSPHIHKEHTTSATSSPYRDTQSKRTASPNRAGKGVIEOTEKSHPR 686

RESULT 4
US-09-739-449-11239
; Sequence 11239, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-101154901C
; CURRENT APPLICATION NUMBER: US/09/739.449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 11239
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-11239

Query Match 10.0%; Score 70; DB 5; Length 509;
Best Local Similarity 25.9%; Pred. No. 2.8;
Matches 36; Conservative 20; Mismatches 59; Indels 24; Gaps 6;

Oy 6 HKKILQLLTGSSDDGHSGLTNSPLDSSCKRSSVSTSPSGVSSSTSG-----G 54
Db 302 HSRLLERAKAKUSDENGAGSLTALPYIET-QGNDVSAFLPTVWISTDQILFLETDLEYQG 360

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OY 55 VSSVSNMGGSLDJEKHHRLHLLLN--GNSAEVAKITTAQT-----CKDVSSTS--CGD 106
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 361 IRPAVNWGLSFRGSAOIKAMQVAGSTIGELAQIREMAAFQFSDIDASTQRLINR 420
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 107 G---NVVKEQLSPKRKE 121
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 421 GARLTLLKQFQFSPKLTE 439
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY

```

```

RESULT      5
US-09-739-449-9535
: Sequence 9535, Application US/09739449
: GENERAL INFORMATION:
: APPLICANT: Hinkle, Gregory J.
: TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
: FILE REFERENCE: 38-10(115490)/C
: CURRENT APPLICATION NUMBER: US/09/739,449
: CURRENT FILING DATE: 2000-12-19
: PRIOR APPLICATION NUMBER: US 09/514,000
: PRIOR FILING DATE: 2000-02-23
: NUMBER OF SEQ ID NOS: 13351
: SEQ ID NO 9535
: LENGTH: 296
: TYPE: PRT
: ORGANISM: Agrobacterium tumefaciens
: US-09-739-449-9535

```

	Query Match	9.5%	Score 66.5;	DB 5;	Length 296;	
	Best Local Similarity	23.9%;	Pred. No.3.2;			
	Matches 28;	Conservative 24;	Mismatches 46;	Indels 19;	Gaps 6;	
QY	4 KGHKLLDLLITCCSSDPRHSSL-TTSPILDSCKESVSYTPSGVSSST---- <td></td> <td></td> <td></td> <td></td> <td></td>					
	: : : : : : : : : : : : : : : : : : :					
Db	26 KGVPRGLAVIVIGNDPASHAYVNSKSKMAKOCGFNSIOHTLTPEETTOALLKLWGEELNTD 85					
	: : : : : : : : : : : : : : : : : : :					
OY	59 SNNHSLLQ-----EKH-----RIHLKKLQ-----NGNSPAEFAKTITAATGCDTSITISC 104					
	: :					
Db	86 ASIHILVALPLPKFNSDEIQTSLIPERDVGLSVLNAGKI--ATGDLAGLGLISL 139					
	: : : : : : : : : : : : : : : : : : :					

```

RESULT      6
US-09-739-449-8471
: Sequence 8471, Application US/09739449
: GENERAL INFORMATION:
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Slater, Steven C.
: TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
: FILE REFERENCE: 38-10(115900)C
: CURRENT APPLICATION NUMBER: US/09/739,449
: CURRENT FILING DATE: 2000-12-19
: PRIOR APPLICATION NUMBER: US 09/514,000
: PRIOR FILING DATE: 2000-02-23
: NUMBER OF SEQ ID NOS: 13351
: SEQ ID NO 8471
: LENGTH: 362
: TYPE: PR1
: ORGANISM: Agrobacterium tumefaciens
: US-09-739-449-8471

```

Query Match	9.2%	Score 65;	DB 5;	Length 382;
Best Local Similarity	23.1%;	Pred. No. 6.1;		
Matches	33;	Conservative	23;	Mismatches 53; Indels 34; Gaps 9;
OY	16	SSDDRGHSSLNPLDSCCKESSVVTSPSG--VSSSTISGCVSSTSMMHGLQEK-NHI	72	
	:::	: : :	:	: : : :
Dd	2	TTDQTPHQTFDPROPFLASENERLLIDIVRRHGRIARSSITG-----HTNLTOOSVHRL	53	
OY	73	LHLKLLONG-----NSPAEVAKITAQAT-----GKRTSSITSC-GD--GNVVKQ	112	
Dd	54	IEALDERILDTGALDKTCRGPPTTIEVLPEPAAVSLSISINTDSVICIADIAFRNCNVYE	113	

QY	113	EQLS--PKKENN-ALLRYLLDR	132
		1: 1: :	
Db	114	EKLMLPEDREETLALSQALDR	136

```

RESULT      7
US-09-739-449-9028
: Sequence 9028, Application US/09739449
:
: GENERAL INFORMATION:
:
: APPLICANT: Hinkle, Gregory J.
:
: TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses thereof
:
: FILE REFERENCE: 38-10115490/C
:
: CURRENT APPLICATION NUMBER: US/09/739,449
:
: CURRENT FILING DATE: 2000-12-19
:
: PRIOR APPLICATION NUMBER: US 09/514,000
:
: PRIOR FILING DATE: 2000-02-23
:
: NUMBER OF SEQ ID NOS: 13351
:
: SEQ ID NO 9028
:
: LENGTH: 787
:
: TYPE: PRT
:
: ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9028

```

```

RESULT      8
US-60-248-505-714
: Sequence 714, Application US/60248505
:
: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
: TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
: TITLE OF INVENTION: PROTEINS, AND USES THEREOF
: FILE REFERENCE: c1000918
: CURRENT APPLICATION NUMBER: US/60/248,505
: CURRENT FILING DATE: 2000-11-15
: NUMBER OF SEQ ID NOS: 1998
:
: SOFTWARE: PasteSeq for windows Version 4.0.
:
: SEQ ID NO 714
:
: LENGTH: 2000
:
: TYPE: PR1
:
: ORGANISM: Human
:
: US-60-248-505-714

```

	Query Match	9.0%	Score 63.5:	DB 6:	Length 2000:	
	Best Local Similarity	23.6%:	Pred. No. 63:			
	Matches	39:	Conservative	24:	Mismatches	51:
					Indels	51:
					Gaps	77:
OY	3 SKGHRKLQLLT-----CSDDRGHSHSLNSPLDSCKESSVY-----	41				
	: :		: :	: :		
Db	159 SYRHEIAPGLTSEWTRTVLTLNRSREAESMPRTSASVLSVLHQEGGSQASY	218				
OY	42 TS-----PGCVSSSTSGGVSNMNGSLQEE-----KHRLHLILO--NGN	81				
	: : : : : : : : : : : : : : : :					
Db	219 TTSATGRGRRFASGLATESGGSGGNSSNNNGSI RHLEOCDLRFFLEYDRLODELDSLSQE	278				
OY	82 SPAEVAKITTAQTGKDTSSITSGGDCNVVKOEQLSPKKENNALL	126				
	: : : : : : : : : : : : : : : :					
Db	279 APQ-----TQQAEQLMNINNIESPGRSH-----QPTRPSSENNSSL	313				
RESULT	9					


```
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 3418 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-421-124-44
```

```
Query Match          9.0%: Score 63; DB 5; Length 3418;
Best Local Similarity 18.6%: Pred. NO. 1.3e+02;
Matches 30; Conservative 29; Mismatches 56; Indels 46; Gaps 6;
```

```
QY 3 SKGHKKLLQLTCCSDDRGHSSLTNSPLDSSCK--ESSVSVTSPGVSSTSGVSSSTS 59
|||:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1263 SKCHDSVSMKRIEN---HNDKTVSEKNNKCQLLQNNIEMTGTVEEITENYKRNTE 1318
```

```
QY 60 N-----MHGS-----LQEKHRIILHKL-----LQNGNS 82
|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1319 NEDNKYTAASRNSHNLEFDGSDSSKNDTVCIHKDETDLFTDQHNICLKLGQFMKEGNT 1378
```

```
QY 83 PAEYAKITAGATGKDTSSITSCGDGNVVKQOLSPKKKENN 123
:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1379 --QIKEDLSLTFLEVAKAQEACHGNTSNKQQLATYATTEON 1417
```

```
RESULT 15
US-09-421-124-44
Sequence 44, Application US/09421124
GENERAL INFORMATION:
APPLICANT: Futreal, Phillip A
APPLICANT: Wooster, Richard F
APPLICANT: Ashworth, Alan
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer
TITLE OF INVENTION: susceptibility gene and uses thereof.
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CITY: Raleigh
STATE: NC
COUNTRY: USA
ZIP: NC 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,124
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
```

```
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 3418 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-421-124-44
```

```
Query Match          9.0%: Score 63; DB 5; Length 3418;
Best Local Similarity 18.6%: Pred. NO. 1.3e+02;
Matches 30; Conservative 29; Mismatches 56; Indels 46; Gaps 6;
```

```
QY 3 SKGHKKLLQLTCCSDDRGHSSLTNSPLDSSCK--ESSVSVTSPGVSSTSGVSSSTS 59
|||:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1263 SKCHDSVSMKRIEN---HNDKTVSEKNNKCQLLQNNIEMTGTVEEITENYKRNTE 1318
```

```
QY 60 N-----MHGS-----LQEKHRIILHKL-----LQNGNS 82
|||:|:|:~|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1319 NEDNKYTAASRNSHNLEFDGSDSSKNDTVCIHKDETDLFTDQHNICLKLGQFMKEGNT 1378
```

```
QY 83 PAEYAKITAGATGKDTSSITSCGDGNVVKQOLSPKKKENN 123
:::|:|:|:|:|:|:|:|:~|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1379 --QIKEDLSLTFLEVAKAQEACHGNTSNKQQLATYATTEON 1417
```

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Search completed: April 19, 2001, 16:54:11
Job time: 495 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2001, 16:50:51 ; Search time 32.49 Seconds
(without alignments)
95.788 Million cell updates/sec

Title: US-09-041-994-2_COPY_1018_1179

Perfect score: 845
Sequence: 1 EQVSHGTGNRRLNLSDDL.....MRPRTPKQLRMQLQRLQ 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCRTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	10.5	415	US-09-176-657-8	Sequence 8, Appl1
2	85.5	10.1	3969	US-08-061-376-5	Sequence 5, Appl1
3	85	10.1	2414	US-08-227-536-2	Sequence 2, Appl1
4	85	10.1	2414	PCR-US95-04682-2	Sequence 2, Appl1
5	84	9.9	357	US-08-612-986-5	Sequence 5, Appl1
6	84	9.9	357	US-08-361-806A-5	Sequence 5, Appl1
7	84	9.9	357	PCR-US95-16806A-5	Sequence 5, Appl1
8	79	9.3	314	US-08-525-742-6	Sequence 6, Appl1
9	75.5	8.9	485	US-08-749-391-2	Sequence 2, Appl1
10	75.5	8.9	485	US-09-390-200-2	Sequence 2, Appl1
11	75	8.9	723	US-08-548-159-5	Sequence 5, Appl1
12	75	8.9	1078	US-08-480-474-11	Sequence 11, Appl1
13	74.5	8.8	510	US-08-278-635B-4	Sequence 4, Appl1
14	74.5	8.8	510	US-08-471-961-4	Sequence 4, Appl1
15	74.5	8.8	1863	US-08-603-753D-2	Sequence 2, Appl1
16	74.5	8.8	1863	US-09-099-753-2	Sequence 2, Appl1
17	74.5	8.8	1863	US-08-986-106-2	Sequence 2, Appl1
18	74.5	8.8	2441	US-08-194-468-2	Sequence 2, Appl1
19	74.5	8.8	2441	US-08-961-739-2	Sequence 2, Appl1
20	74	8.8	511	US-08-464-258B-4	Sequence 4, Appl1
21	73.5	8.7	241	US-08-867-087B-11	Sequence 11, Appl1
22	72.5	8.6	301	US-08-785-464-1	Sequence 1, Appl1
23	72.5	8.6	381	US-09-135-021-80	Sequence 80, Appl1
24	72.5	8.6	676	US-09-135-021-2	Sequence 2, Appl1
25	72.5	8.6	765	US-08-425-061-19	Sequence 19, Appl1
26	72.5	8.6	765	US-08-825-886-19	Sequence 19, Appl1
27	72.5	8.6	864	US-08-620-694A-2	Sequence 2, Appl1

28	72.5	8.6	864	US-09-022-255-2	Sequence 2, Appl1
29	72.5	8.6	864	US-09-022-696-2	Sequence 2, Appl1
30	72.5	8.6	864	US-08-978-773-2	Sequence 2, Appl1
31	72.5	8.6	864	US-09-022-253-2	Sequence 2, Appl1
32	72.5	8.6	864	US-09-022-260-2	Sequence 2, Appl1
33	72.5	8.6	864	US-09-022-259-2	Sequence 2, Appl1
34	72.5	8.6	864	US-09-022-257-2	Sequence 2, Appl1
35	72.5	8.6	900	US-08-425-061-20	Sequence 20, Appl1
36	72.5	8.6	900	US-08-825-886-20	Sequence 20, Appl1
37	72.5	8.6	914	US-08-425-061-21	Sequence 21, Appl1
38	72.5	8.6	914	US-08-825-886-21	Sequence 21, Appl1
39	72.5	8.6	1202	US-08-425-061-22	Sequence 22, Appl1
40	72.5	8.6	1202	US-08-825-886-22	Sequence 22, Appl1
41	72.5	8.6	1363	US-08-425-061-23	Sequence 23, Appl1
42	72.5	8.6	1363	US-08-825-886-23	Sequence 23, Appl1
43	72.5	8.6	1852	US-08-425-061-24	Sequence 24, Appl1
44	72.5	8.6	1852	US-08-825-886-24	Sequence 24, Appl1
45	72.5	8.6	1863	US-08-425-061-16	Sequence 16, Appl1

ALIGNMENTS

```
RESULT 1
US-09-176-657-8
; Sequence 8, Application US/09176657
; Patent No. 6020164
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/176,657
; CURRENT FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; OTHER INFORMATION: g608464
US-09-176-657-8

Query Match 10.5%; Score 89; DB 3; Length 415;
Best Local Similarity 30.3%; Pred. No. 0.067;
Matches 40; Conservative 17; Mismatches 41; Indels 34; Gaps 7;

QY 36 LLDOLHTLSTNTATGEEIDRALGI-----PELVNQGALRP--KODFOGGEAAVMM 87
Db 242 ILDOQNPMLMOASLAIAOQNNRALLRSPLVAOSLGRGPAIIPGQCPFFQLQALAA-- 299
QY 88 DOKAGLYGQTYPPAGPQMGCFHLGQSPFSNMMNOMN--QOGNFPLOGMHRIMRP 145
Db 300 -----GNPLA---QLQGPPLEFNAAALQTNALQGSAP---GMDPNAVIALA 339
QY 146 RYTPKQLRMQL 157
Db 340 LAN--EQARFQL 349

RESULT 2
US-08-061-376-5
; Sequence 5, Application US/08061376
; Patent No. 6175000
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Djabali, Malek
```

```

1  APPLICANT: Selter, Lucia
2  APPLICANT: Parry, Pauline
3  TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11Q23
4  TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS
5  NUMBER OF SEQUENCES: 12
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
8  STREET: 444 South Flower Street, Suite 2000
9  CITY: Los Angeles
10 STATE: California
11 COUNTRY: USA
12 ZIP: 90071
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patentln Release #1.0, Version #1.25
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/061,376
22 FILING DATE: 13-MAY-1993
23 CLASSIFICATION: 435
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Relter, Stephen E.
26 REGISTRATION NUMBER: 31,192
27 REFERENCE/DOCKET NUMBER: P41 9387
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (619)546-4737
30 TELEFAX: (619)546-9392
31 INFORMATION FOR SEQ ID NO: 5:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 3969 amino acids
34 TYPE: amino acid
35 STRANDEDNESS: unknown
36 TOPOLOGY: unknown
37 MOLECULE TYPE: protein
38
39 US-061-376-5
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COMPUTER READABLE FORM:
MEDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,536
FILING DATE: 14-APR-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: DPCI-308XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 543-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2414 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-227-536-2

Query Match          10.1%; Score 85; DB 1; Length 2414;
Best Local Similarity 23.5%; Pred. No. 2.4;
Matches 44; Conservative 16; Mismatches 57; Indels 70; Gaps 7;

OY      6 GTGNNPLRLNSLDDLVGPSNLEGSDERALDQLHTLLSTNDATNGEIDRALCIPELY 65
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::|
Db      2044 GTVSOQALQNLRLTRSPSSPLQQQ---VLSTH-----ANPQLL 2081

OY      66 NQGALPEPKODAFQGEAEAVMDOKAGLYGTYPACGP-----PMGG 108
       |::||::||::||::||::||::||::||::||::||::||::||::||::||::|
Db      2082 -----AFLTKQAARTANSNPRIEGQPCMPGCGELCPPTMPGQOG 2123

OY      109 PHLGQSFSFNSM-----NMNQGNFPLQGMHRANIRPRTNT-PKOLR--M 155
       :||::||::||::||::||::||::||::||::||::||::||::||::||::|
Db      2124 VHSNPNAMNMNMQGVORAGLPQQQPQQQLPPMGSGMSPPQAQNMNMHWTPSQFRDL 2183

OY      156 QLOQRLO 162
       ::||::|
Db      2184 RROQMWO 2190

RESULT      4
PCT-US95-04682-2
Sequence 2, Application PC/TUS9504682
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: NUCLEIC ACID ENCODING TRANSCRIPTION
TITLE OF INVENTION: FACTOR P300 AND USES OF P300
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04682
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,536
FILING DATE: 14-April-1994
```

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Holliday C. Helne, Ph. D.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFCT-308X999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2414 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04682-2

Query Match 10.1%; Score 85; DB 5; Length 2414;
Best Local Similarity 23.5%; Pred. No. 2.4;
Matches 44; Conservative 16; Mismatches 57; Indels 70; Gaps 7;

QY 6 GTGNRLRLMSLDLVGPSNLEGSDEKALDQLHTLSNTDATGTEIDRALGPELV 65
DB 2044 GTVSGQALONLRLTSPSSPLQOOO-VLSILH-ANPOL 2081
QY 66 NCGALEPPKQDAFGQGEAAVMDOKAGLYGQYPAQGP-PMQGG 108
DB 2082 -AAFIKORAKYANSNPQPIFGQPGMPQGPGLQPTMPEGQG 2123
QY 109 FHLQSGSPFSNSM-MNQMNQGNFPLQSMHPRANIMRPTNT-PKQLR-M 155
DB 2124 VHSNPMQNNPNQAGVQRAGLRQQQDQQLQDPFMGMSPPQAOQMNHNHTMNSQFRLDIL 2183
QY 156 QLQQRLLQ 162
DB 2184 RROQMMD 2190

RESULT 5
US-08-612-986-5
Sequence 5, Application US/08612986
Patent No. 5770384
GENERAL INFORMATION:
APPLICANT: Elliot J. Androphy
TITLE OF INVENTION: E2 BINDING PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,986
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/361,806
FILING DATE: 22 DEC 1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: NEP-004DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-612-986-5

Query Match 9.9%; Score 84; DB 1; Length 357;
Best Local Similarity 27.0%; Pred. No. 0.2;
Matches 33; Conservative 6; Mismatches 47; Indels 36; Gaps 3;

QY 73 PKQDAFGQGE-AAVMDOKAGLYGQYPAQGP- 103
DB 199 PEHGQFGQSGAYGTRQPPHYGPTQPAVSPQQLRAPSAPAVOYLQSORQHPAVNHG 258
QY 104 -PMQGGFHLQSGSPFSNSMNMNQGNF-PLQGMHPRANIMRPTNTPKQLRMD 156
DB 259 HFGPTQFGFLQPGALSLQKQMEHANOQTFSDSSSLRPMHQRALLPAPOLLASPOLPQV 318
QY 157 LQ 158
DB 319 MQ 320

RESULT 6
US-08-361-806A-5
Sequence 5, Application US/08361806A
Patent No. 5792833
GENERAL INFORMATION:
APPLICANT: Elliot J. Androphy
TITLE OF INVENTION: E2 BINDING PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,806A
FILING DATE: 22 DEC 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: NEP-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-361-806A-5

Query Match 9.9%; Score 84; DB 1; Length 357;
Best Local Similarity 27.0%; Pred. No. 0.2;
Matches 33; Conservative 6; Mismatches 47; Indels 36; Gaps 3;

QY 73 PKQDAFGQGE-AAVMDOKAGLYGQYPAQGP- 103

TITLE OF INVENTION: Anaerobic Fungus
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: USA
ZIP: 80803
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,391
FILING DATE: 13-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Donna M. Ferber
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 93-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-391-2

Query Match 8.9%; Score 75.5; DB 2; Length 485;
Best Local Similarity 37.9%; Pred. No. 2.7;
Matches 25; Conservative 2; Mismatches 32; Indels 7; Gaps 2;

QY 88 DQKAGLYGQYTPAQGPMPGCGFHLQGSFNSMNMNMN-QQGNFPLQGNHPRANITMRPR 146
DB 268 DQPGGPGGQPPGQGPQGGQPPGQGPQGGQPPGQNDQGGQPPGQGP-----PQ 321
QY 147 TNPQK 152
DB 322 GNDQDQ 327

RESULT 10
US-09-390-200-2
Sequence 2, Application US/09390200
Patent No. 6137032
GENERAL INFORMATION:
APPLICANT: Cheng, Kuo-Joan
APPLICANT: Selienger, Leonard B.
APPLICANT: Liu, Jin-Hao
APPLICANT: Hu, Youji
APPLICANT: Forsberg, Cecil W.
APPLICANT: Moloney, Maurice M.
TITLE OF INVENTION: A xylanase Obtained From an
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: USA
ZIP: 80803
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/390,200
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/749,391
FILING DATE: 13-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Donna M. Ferber
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 93-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-390-200-2

Query Match 8.9%; Score 75.5; DB 4; Length 485;
Best Local Similarity 37.9%; Pred. No. 2.7;
Matches 25; Conservative 2; Mismatches 32; Indels 7; Gaps 2;

QY 88 DQKAGLYGQYTPAQGPMPGCGFHLQGSFNSMNMNMN-QQGNFPLQGNHPRANITMRPR 146
DB 268 DQPGGPGGQPPGQGPQGGQPPGQGPQGGQPPGQNDQGGQPPGQGP-----PQ 321
QY 147 TNPQK 152
DB 322 GNDQDQ 327

RESULT 11
US-08-548-159-5
Sequence 5, Application US/08548159
Patent No. 5989511
GENERAL INFORMATION:
APPLICANT: MacLaren, No. 5989511 K.
APPLICANT: No. 5989511kins, Abner L.
APPLICANT: Lan, Michael S.
APPLICANT: Li, Qing
TITLE OF INVENTION: Materials and Methods for Detection and
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/548,159
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UP154.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-375-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

DB 428 -----MEPETHPSQASEILLSPQIOKALE 452

RESULT 14
US-08-471-961-4

; Sequence 4, Application US/08471961

; Patent No. 6100046

; GENERAL INFORMATION:

; APPLICANT: ELGOYHEN, ANA BELEN

; APPLICANT: JOHNSON, DAVID S.

; APPLICANT: BOUTLER, JAMES R.

; APPLICANT: HEINEMANN, STEPHEN F.

; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL

; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GRAY CARY WARE & FREIDENRICH

; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600

; CITY: SAN DIEGO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/471,961

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/278,635

; FILING DATE: 21-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: REITER, STEPHEN E.

; REGISTRATION NUMBER: 31,192

; REFERENCE/DOCKET NUMBER: P41 9771

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-677-1409

; TELEFAX: 619-677-1465

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 510 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-471-961-4

Query Match 8.8%; Score 74.5; DB 3; Length 510;

Best Local Similarity 22.7%; Pred. No. 3.7;

Matches 37; Conservative 13; Mismatches 36; Indels 77; Gaps 8;

QY 9 NRPLRLNSDDLVGPSNLESGOSDERALLDQLHTLLSNLDATGLEGIDRALGIPELVNG 68

DB 358 NRPLRLNSDDLVGPSNLESGOSDERALLDQLHTLLSNLDATGLEGIDRALGIPELVNG 68

QY 69 QALEPKQDAFOGCEAV---MMDOKAG-LYQGTYPAGCPMOGPFHLOGQSPFSNMNQ 124

DB 389 ERETEEEEDENICVACGLPDSSMGVLYG-----HGHLRA----- 427

QY 125 MNOQGNFPLQGMHRANIRPTNTPKQ-----LRMOLOQRLO 162

DB 428 -----MEPETHPSQASEILLSPQIOKALE 452

RESULT 15

US-08-603-753D-2

; Sequence 2, Application US/08603753D

; Patent No. 5891857

; GENERAL INFORMATION:

APPLICANT: HOLT, JEFFREY T.

APPLICANT: JENSEN, ROY A.

APPLICANT: PAGE, DAVID L.

APPLICANT: KING, MARY-CLAIRE

APPLICANT: SZABO, CSILLA I.

APPLICANT: JETTON, THOMAS L.

APPLICANT: ROBINSON-BENION, CHERYL L.

APPLICANT: THOMPSON, MARILYN E.

; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2

; TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARLES A. TAYLOR, JR

; STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER

; STREET: BOULEVARD

; CITY: DURHAM

; STATE: NORTH CAROLINA

; COUNTRY: USA

; ZIP: 27707

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage

; COMPUTER: IBM PC/XT/AT compatible

; OPERATING SYSTEM: Windows 3.1

; SOFTWARE: WORD PERFECT 6.1 and ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/603,753D

; FILING DATE: 20 FEB 1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/373,799

; FILING DATE: 17 JAN 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: ARLES A. TAYLOR, JR.

; REGISTRATION NUMBER: 39,395

; REFERENCE/DOCKET NUMBER: 1242/2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919) 493-8000

; TELEFAX: (919) 419-0383

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1863

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; HYPOTHETICAL: no

; ANTI-SENSE: no

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE: adult

; TISSUE TYPE: female breast

; CELL TYPE: ductal carcinoma in situ, invasive

; CELL LINE: not derived from a cell line

; ORGANELLER: no

; IMMEDIATE SOURCE:

; LIBRARY: cDNA library derived from human

; CLONE: obtained using published sequence

; POSITION IN GENOME:

; CHROMOSOME/SEGMENT: unknown

; MAP POSITION: unknown

; UNITS: unknown

; FEATURE:

; NAME/KEY: BRCA1 protein

; LOCATION: 1 to 1863

; IDENTIFICATION METHOD: observation of mRNA and

; IDENTIFICATION METHOD: antisense inhibition of BRCA1 gene

; OTHER INFORMATION: BRCA1 protein has a negative

; OTHER INFORMATION: regulatory effect on growth of human mammary cells.

; PUBLICATION INFORMATION:

AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
 ovarian cancer susceptibility gene BRCA1.
JOURNAL: Science
VOLUME: 266
PAGES: 66-71
DATE: 1994
RELEVANT RESIDUES IN SEQ ID NO: 2: granin box
RELEVANT RESIDUES IN SEQ ID NO: domain at amino acids 1214-1223
US-08-603-753D-2

Query Match 8.88; Score 74.5; DB 2; Length 1863;
Best Local Similarity 22.58; Pred. No. 24;
Matches 36; Conservative 30; Mismatches 71; Indels 23; Gaps 7;
QY 18 DDLVPPSNLEGGSDERALLDQLHTLSNTD--ATGLEIDRALGIPELVNOGQALEPKQ 75
Db 390 DELGSDSDSHDGESESNKAVADVLDVNEVDYSGSSSEKIDLASDPH-----EALICKS 444
QY 76 DAFQGGQEAAYMMQKAGLYGQTY--PAQGPWQ-----GGFHLGGQSPSPFNSMMNQ 125
Db 445 DRVHSK--SVESDIEDKIFGKTYRKASLPNLSHTVENLIGAFVSEPOIIQERPLTNKL 502
QY 126 NQGGNFPILGWHPRANIMRPR--TNTPKQLRMQLQRLQ 162
Db 503 KRKR-PTSGLHPEDEIKKADLAVOKTPEMINQGTNQTQ 541

Search completed: April 19, 2001, 16:50:54
Job time: 302 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2001, 16:54:03 ; Search time 147.68 Seconds
(without alignments)
176.452 Million cell updates/sec

Title: US-09-041-994-2_COPY_1018_1179

Perfect score: 845

Sequence: 1 EGVSHGTQNPRLRLNSLDDL.....MRPRTNPKQLRMQLQRLQ 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1009251 seqs, 160854530 residues

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/2/paa/PCRTUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
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20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	845	100.0	951	US-09-125-635-8	Sequence 8, Appli
2	845	100.0	1415	US-09-041-994-2	Sequence 2, Appli
3	845	100.0	1415	US-09-513-066-2	Sequence 2, Appli
4	845	100.0	1420	US-09-125-635-4	Sequence 4, Appli
5	761	90.1	1402	US-09-125-635-12	Sequence 12, Appli
6	757	89.6	1398	US-09-513-066-14	Sequence 14, Appli
7	757	89.6	1402	US-09-445-353A-2	Sequence 2, Appli
8	564.5	66.8	1391	US-09-513-066-15	Sequence 15, Appli
9	312.5	37.0	1127	US-60-258-273-113	Sequence 113, App
10	312.5	37.0	1464	US-08-891-640-2	Sequence 2, Appli

11	310.5	36.7	1462	18	US-09-445-353A-3	Sequence 3, Appli
12	278	32.9	58	12	US-08-891-640-9	Sequence 9, Appli
13	266.5	31.5	1036	12	US-08-891-640-3	Sequence 3, Appli
14	266.5	31.5	1061	11	US-08-701-154A-5	Sequence 5, Appli
15	237	28.0	51	23	US-60-160-189-8436	Sequence 8436, Ap
16	237	28.0	51	23	US-60-169-867-5713	Sequence 5713, Ap
17	104	12.3	5222	23	US-60-245-201-208	Sequence 208, App
18	98.5	11.7	2247	23	US-60-167-217-16010	Sequence 16010, A
19	98.5	11.7	2247	23	US-60-173-464-13121	Sequence 13121, A
20	98.5	11.7	2285	23	US-60-191-637-16007	Sequence 16007, A
21	98.5	11.7	2285	23	US-60-191-637-12683	Sequence 12683, A
22	93	11.0	863	16	US-09-252-991A-21831	Sequence 21831, A
23	92.5	10.9	185	23	US-60-196-718-6866	Sequence 6866, Ap
24	91.5	10.8	275	21	US-09-733-089-18395	Sequence 18395, A
25	91	10.8	333	16	US-09-270-767-38937	Sequence 38937, A
26	91	10.8	333	16	US-09-270-767-54154	Sequence 54154, A
27	90.5	10.7	800	23	US-60-167-217-18636	Sequence 18636, A
28	90.5	10.7	800	23	US-60-173-464-15281	Sequence 15281, A
29	90.5	10.7	816	23	US-60-191-637-18596	Sequence 18596, A
30	90.5	10.7	816	23	US-60-191-681-14717	Sequence 14717, A
31	90	10.7	506	20	US-09-619-049-879	Sequence 879, App
32	90	10.7	506	23	US-60-167-217-17261	Sequence 17261, A
33	90	10.7	506	23	US-60-171-627-1365	Sequence 1365, Ap
34	90	10.7	506	23	US-60-173-464-14141	Sequence 14141, A
35	90	10.7	506	23	US-60-191-637-17261	Sequence 17261, A
36	90	10.7	506	23	US-60-191-681-13664	Sequence 13664, A
37	90	10.7	1572	23	US-60-224-729-2	Sequence 2, Appli
38	89	10.5	131	23	US-60-197-873-13405	Sequence 13405, A
39	89	10.5	259	23	US-60-167-217-10712	Sequence 10712, A
40	89	10.5	259	23	US-60-173-464-8662	Sequence 8662, Ap
41	89	10.5	259	23	US-60-191-637-10718	Sequence 10718, A
42	89	10.5	259	23	US-60-191-681-8396	Sequence 8396, Ap
43	89	10.5	415	18	US-09-421-239-8	Sequence 8, Appli
44	88.5	10.5	131	23	US-60-197-873-13419	Sequence 13419, A
45	88.5	10.5	152	23	US-60-197-873-13417	Sequence 13417, A

ALIGNMENTS

RESULT 1

US-09-125-635-8

Sequence 8, Application US/09125635

GENERAL INFORMATION:

APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE

TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator

FILE REFERENCE: 49944

CURRENT APPLICATION NUMBER: US/09/125, 635

PRIOR APPLICATION NUMBER: 1998-08-21

PRIOR FILING DATE: 1997-06-17

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 951

TYPE: PRT

ORGANISM: Homo sapiens

US-09-125-635-8

Query Match	Score	DB 15:	Length
Best Local Similarity	100.0%	Pred. No. 1.5e-79;	
Matches 162; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;

QY 1 EGVSHGTQNPRLRLNSLDDLVCPPNMLECOSDRALLDQHTLLSTWDTGTEIDRALG 60

DB 719 EGVSHGTQNPRLRLNSLDDLVCPPNMLECOSDRALLDQHTLLSTWDTGTEIDRALG 778

QY 61 IPELVNQGALFEKODAFQGOEAAVMDQKAGLYGQTYRACGPRMGGFNLGQSPSPNS 120

DB 779 IPELVNQGALFEKODAFQGOEAAVMDQKAGLYGQTYRACGPRMGGFNLGQSPSPNS 838

QY 121 MNQMNOGQNFPLDQGNHPRANIMRPRTNPKQLRMQLQRLQ 162

```
Db 839 MNQMNQGNFPLQGMHPRANIMRPTNTPKQLRMQLQORLQ 880
|||||
RESULT 2
US-09-041-994-2
; Sequence 2, Application US/09041994
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; APPLICANT: Li, Hui
; TITLE OF INVENTION: Transcriptional Coactivator for Nuclear
; TITLE OF INVENTION: Hormone Receptors
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lanhive and Cockfield
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,994
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Liepmann, W. Hugo
; REGISTRATION NUMBER: 20,407
; REFERENCE/DOCKET NUMBER: UMM-026-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-227-7400
; TELEFAX: 617-742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-041-994-2

Query Match 100.0%; Score 845; DB 14; Length 1415;
Best Local Similarity 100.0%; Pred. No. 2,7e-79;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGVSHGTQNRPLRNSLDDLVGPPSNLEGQSDERALLDQLHTLLSNTDATGLEETDRALG 60
|||||
Db 1018 EGVSHGTQNRPLRNSLDDLVGPPSNLEGQSDERALLDQLHTLLSNTDATGLEETDRALG 1077
QY 61 IPELVNQGQALEPKQDAFGQGEAAVMDQKAGLYGQTPAGQPPMGQGFHLOGQSPSPNS 120
|||||
Db 1078 IPELVNQGQALEPKQDAFGQGEAAVMDQKAGLYGQTPAGQPPMGQGFHLOGQSPSPNS 1137
QY 121 MNQMNQGNFPLQGMHPRANIMRPTNTPKQLRMQLQORLQ 162
|||||
Db 1138 MNQMNQGNFPLQGMHPRANIMRPTNTPKQLRMQLQORLQ 1179

RESULT 3
US-09-513-066-2
; Sequence 2, Application US/09513066
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; APPLICANT: Leo, Christopher
; APPLICANT: Li, Hui
; TITLE OF INVENTION: NOVEL USES FOR THE RAC3 TRANSCRIPTIONAL COACTIVATOR OF
; TITLE OF INVENTION: STEROID NUCLEAR RECEPTORS
; FILE REFERENCE: UMG-026CP
; CURRENT APPLICATION NUMBER: US/09/513,066
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; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: USSN 09/041,994
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: USSN 60/073,674
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-066-2

Query Match 100.0%; Score 845; DB 19; Length 1415;
Best Local Similarity 100.0%; Pred. No. 2,7e-79;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGVSHGTQNRPLRNSLDDLVGPPSNLEGQSDERALLDQLHTLLSNTDATGLEETDRALG 60
|||||
Db 1018 EGVSHGTQNRPLRNSLDDLVGPPSNLEGQSDERALLDQLHTLLSNTDATGLEETDRALG 1077
QY 61 IPELVNQGQALEPKQDAFGQGEAAVMDQKAGLYGQTPAGQPPMGQGFHLOGQSPSPNS 120
|||||
Db 1078 IPELVNQGQALEPKQDAFGQGEAAVMDQKAGLYGQTPAGQPPMGQGFHLOGQSPSPNS 1137
QY 121 MNQMNQGNFPLQGMHPRANIMRPTNTPKQLRMQLQORLQ 162
|||||
Db 1138 MNQMNQGNFPLQGMHPRANIMRPTNTPKQLRMQLQORLQ 1179

RESULT 4
US-09-125-635-4
; Sequence 4, Application US/09125635
; GENERAL INFORMATION:
; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
; FILE REFERENCE: 49944
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-125-635-4

Query Match 100.0%; Score 845; DB 15; Length 1420;
Best Local Similarity 100.0%; Pred. No. 2,7e-79;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGVSHGTQNRPLRNSLDDLVGPPSNLEGQSDERALLDQLHTLLSNTDATGLEETDRALG 60
|||||
Db 1018 EGVSHGTQNRPLRNSLDDLVGPPSNLEGQSDERALLDQLHTLLSNTDATGLEETDRALG 1077
QY 61 IPELVNQGQALEPKQDAFGQGEAAVMDQKAGLYGQTPAGQPPMGQGFHLOGQSPSPNS 120
|||||
Db 1078 IPELVNQGQALEPKQDAFGQGEAAVMDQKAGLYGQTPAGQPPMGQGFHLOGQSPSPNS 1137
QY 121 MNQMNQGNFPLQGMHPRANIMRPTNTPKQLRMQLQORLQ 162
|||||
Db 1138 MNQMNQGNFPLQGMHPRANIMRPTNTPKQLRMQLQORLQ 1179

RESULT 5
US-09-125-635-12
; Sequence 12, Application US/09125635
; GENERAL INFORMATION:
; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
```

```
; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
; FILE REFERENCE: 49944
; CURRENT APPLICATION NUMBER: US/09/125,635
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1402
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-125-635-12
```

```
Query Match          90.1%; Score 761; DB 15; Length 1402;
Best Local Similarity 89.5%; Pred. No. 1.7e-70;
Matches 145; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
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```
OY 1 EGVSHGTGNRPLRLNSLDLVPSPNLEGGSDERALLDQHTLLSNTDGTGLEIDRALG 60
DB 1029 EGGPHGSQNRPLRLNSLDLGLPPSNAGSGSDERALLDQHTLLSNTDGTGLEIDRALG 1088
OY 61 IPELVNQGALPEPKODAFQGOEAAVMMQKAGLYGOTYPAQGPMMOGGFHLQGSFSPNS 120
DB 1089 IPELVNQGALPEPKODAFQGOEAAVMMQKAGLYGOTYPAQGPMMOGGFHLQGSFSPNS 1148
OY 121 MMNQMNQGNFPLQGMHPRANIMRPTNTPKQLRMQLQORLQ 162
DB 1149 MMQOISQGSFPLQGMHPRAGLVPRPTNTPKQLRMQLQORLQ 1190
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```
RESULT 6
US-09-513-066-14
; Sequence 14, Application US/09513066
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; APPLICANT: Leo, Christopher
; APPLICANT: Li, Hui
; TITLE OF INVENTION: NOVEL USES FOR THE RAC3 TRANSCRIPTIONAL COACTIVATOR OF
; FILE REFERENCE: UMG-026CP
; CURRENT APPLICATION NUMBER: US/09/513,066
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: USSN 09/041,994
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: USSN 60/073,674
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-066-14
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Query Match          89.6%; Score 757; DB 19; Length 1398;
Best Local Similarity 88.9%; Pred. No. 4.6e-70;
Matches 144; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
```

```
OY 1 EGVSHGTGNRPLRLNSLDLVPSPNLEGGSDERALLDQHTLLSNTDGTGLEIDRALG 60
DB 1025 EGGPHGSQNRPLRLNSLDLGLPPSNAGSGSDERALLDQHTLLSNTDGTGLEIDRALG 1084
OY 61 IPELVNQGALPEPKODAFQGOEAAVMMQKAGLYGOTYPAQGPMMOGGFHLQGSFSPNS 120
DB 1085 IPELVNQGALPEPKODAFQGOEAAVMMQKAGLYGOTYPAQGPMMOGGFHLQGSFSPNS 1144
OY 121 MMNQMNQGNFPLQGMHPRANIMRPTNTPKQLRMQLQORLQ 162
DB 1145 MMQOISQGSFPLQGMHPRAGLVPRPTNTPKQLRMQLQORLQ 1186
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```
RESULT 7
US-09-445-353A-2
; Sequence 2, Application US/09445353A
; GENERAL INFORMATION:
; APPLICANT: Rosenfeld, et al., Michael
; TITLE OF INVENTION: A Transcription Factor Coactivator Protein, p/CIP
; FILE REFERENCE: 6627-PA1021
; CURRENT APPLICATION NUMBER: US/09/445,353A
; CURRENT FILING DATE: 1998-06-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1402
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-445-353A-2
```

```
Query Match          89.6%; Score 757; DB 18; Length 1402;
Best Local Similarity 88.9%; Pred. No. 4.6e-70;
Matches 144; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
```

```
OY 1 EGVSHGTGNRPLRLNSLDLVPSPNLEGGSDERALLDQHTLLSNTDGTGLEIDRALG 60
DB 1025 EGGPHGSQNRPLRLNSLDLGLPPSNAGSGSDERALLDQHTLLSNTDGTGLEIDRALG 1084
OY 61 IPELVNQGALPEPKODAFQGOEAAVMMQKAGLYGOTYPAQGPMMOGGFHLQGSFSPNS 120
DB 1085 IPELVNQGALPEPKODAFQGOEAAVMMQKAGLYGOTYPAQGPMMOGGFHLQGSFSPNS 1144
OY 121 MMNQMNQGNFPLQGMHPRANIMRPTNTPKQLRMQLQORLQ 162
DB 1145 MMQOISQGSFPLQGMHPRAGLVPRPTNTPKQLRMQLQORLQ 1186
```

```
RESULT 8
US-09-513-066-15
; Sequence 15, Application US/09513066
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; APPLICANT: Leo, Christopher
; APPLICANT: Li, Hui
; TITLE OF INVENTION: NOVEL USES FOR THE RAC3 TRANSCRIPTIONAL COACTIVATOR OF
; FILE REFERENCE: UMG-026CP
; CURRENT APPLICATION NUMBER: US/09/513,066
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: USSN 09/041,994
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: USSN 60/073,674
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-066-15
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Query Match          66.8%; Score 564.5; DB 19; Length 1391;
Best Local Similarity 71.9%; Pred. No. 7.2e-50;
Matches 115; Conservative 17; Mismatches 25; Indels 3; Gaps 3;
```

```
OY 6 GTGNRPLRLNSLDLVPSPNLEGGSDERALLDQHTLLSNTDGTGLEIDRALGIPELY 65
DB 1014 GAQNRPLGRNSLDLGLCPSTVYGQDTETALLDQHTLLSNTDGTGLEIDRALGIPDLY 1073
OY 66 NQGOALEPKODAFQGOEAAVMMQKAGLYGOTYPAQGPMMQ-GGF-HLQGSFSPNSMKN 123
DB 1074 SQGOALEPKODAFQGOEAAVMMQKAGLYGOTYPAQGPMMQ-GGF-HLQGSFSPNSMKN 1133
```


APPLICANT: Lutz, Yves
TITLE OF INVENTION: Transcriptional Intermediary Factor-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,640
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,247
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1383.0130001/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-891-640-9

Query Match 32.9%; Score 278; DB 12; Length 58;
Best Local Similarity 94.8%; Pred. No. 8.3e-22;
Matches 55; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 LKNSLDDLVGPPSNLEGOSDERALDQLHTLSNTDATGTEIDRALGIPELVNOGA 70
DB 1 LKNSLDDLVGPPSNLEGOSDERALDQLHTLSNTDATGTEIDRALGIPELVNOGA 58

RESULT 13
US-08-891-640-3
Sequence 3, Application US/08891640
GENERAL INFORMATION:
APPLICANT: Chamdon, Pierre
APPLICANT: Gronmeyer, Hinrich
APPLICANT: Voegel, Johannes
APPLICANT: Lutz, Yves
TITLE OF INVENTION: Transcriptional Intermediary Factor-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,640
FILING DATE: Herewith

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,247
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1383.0130001/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-891-640-3

Query Match 31.5%; Score 266.5; DB 12; Length 1036;
Best Local Similarity 42.5%; Pred. No. 8.9e-19;
Matches 68; Conservative 28; Mismatches 49; Indels 15; Gaps 7;

QY 13 LKNSLDDLVGPPSNLEGOSDERALDQLHTLSNTDATGTEIDRALGIPELVNOGALE 72
DB 535 ISSQLDELCPPTVYEGNDERALLLEQLVSLGKDETELAEIDRALGIDKLVLGGGLD 593

QY 73 PKDAFQGOEAA--VMADQKAGLYGQTYPAQGP-----PMGGFHLQGSQSFNSMMNQ 124
DB 594 VLSEFRPQQAATPPLIMERPNLYSQPYSSPPTANLPSFPG---MVRKRSLSGTMPQ 650

QY 125 MN-QQGNF-PLOGMHPRANIMPRNTPKOLRNQLOQRLO 162
DB 651 VTPRGAFSPGMQMPQRTLNRPAA-APNQLRLQLOQRLO 689

RESULT 14
US-08-701-154A-5
Sequence 5, Application US/08701154A
GENERAL INFORMATION:
APPLICANT: Tsai, Ming-Jer
APPLICANT: Tsai, Sophia Y.
APPLICANT: Onate, Sergio A.
TITLE OF INVENTION: STEROID RECEPTOR COACTIVATOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,154A
FILING DATE: August 21, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/003,784
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 220/243
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1061 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-701-154A-5

Query Match 31.5%; Score 266.5; DB 11; Length 1061;

Best Local Similarity 42.5%; Pred. No. 9.3e-19;

Matches 68; Conservative 28; Mismatches 49; Indels 15; Gaps 7;

QY 13 LRNSLDLVGPPSNLEGSODERALDDQLHTLLSNTDATGLEIDRALGIPELVNOGALE 72

Db 529 ISSOLDELICPPTVEGGRNDEKALLEQLVSLSGKDETELAEIDRALGIDKLIV-QGGGLD 587

QY 73 PKDAFQGGQEA--VMNQKAGLVGQTPPAQGP-----PMQGGFHLQGSFNSMMNQ 124

Db 588 VLSEFPPOQATPPLIMEERNLYSQPYSSPPTANLPSPFG--WVRQKPSLGTMPVQ 644

QY 125 MN-QQGNF-PLQGMFRANIMRPTNTPKQLRMQLQQRILQ 162

Db 645 VTPRGAFSPGMGMQPROTLNRPPA-APNQLRLQLQQRILQ 683

RESULT 15

US-60-160-189-8436

; Sequence 8436, Application US/60160189

; GENERAL INFORMATION:

; APPLICANT: BONAZZI, VIVIEN

; TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: C1000112

; CURRENT APPLICATION NUMBER: US/60/160,189

; CURRENT FILING DATE: 1999-10-19

; NUMBER OF SEQ. ID NOS: 10162

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ. ID NO 8436

; LENGTH: 51

; TYPE: PRT

; ORGANISM: HUMAN

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)..(51)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-60-160-189-8436

Query Match 28.0%; Score 237; DB 23; Length 51;

Best Local Similarity 92.2%; Pred. No. 1.4e-17;

Matches 47; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 NRPLLRNSLDLVGPPSNLEGSODERALDDQLHTLLSNTDATGLEIDRAL 59

Db 1 SRPLLRNSLDLVGPPSTLEGSODERALDDQHTLVSNMTDATGLEIDRAL 51

Search completed: April 19, 2001, 16:54:06
Job time: 493 sec

[illegible]

FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 8151
LENGTH: 407
TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-09-739-449-8151

Query Match 7.4%; Score 62.5; DB 5; Length 407;
Best Local Similarity 23.5%; Pred. No. 11;
Matches 39; Conservative 20; Mismatches 58; Indels 49; Gaps 8;

QY 12 LIRNSLDLVGPPSNLEGSQSDERALLDQLHTLLSNTDATGLEIDRALGIPELVNOG-A 70
DB 44 ILRGALDGLTAVPP--VGDPEYALRQOL-FLRTEGEN-----PALALDGYFA 88
QY 71 LEPR-----QDAFGGGEAAVMDQKAGLYGQTPPAOGPPMOGFGHLOG--QSFNSMNMQ 124
DB 89 LHPSLRNFRRLYRKGEAAVHASATGYDRSHFDGQDYLESGFATPGHVESGMLNRLLEQ 148
QY 125 MNO-----OGNFPLOGMHPRANIMRP 145
DB 149 MPAGETIPNAGADRVYSGIATGASAPLVIRGKAPILGMAP--SVLRP 192

RESULT 7
US-09-661-322A-28
Sequence 28, Application US/09661322A
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Rupert, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
FILE OF INVENTION: and Methods of Use
FILE REFERENCE: MECO201
CURRENT APPLICATION NUMBER: US/09/661,322A
CURRENT FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.0
SEQ ID NO 28
LENGTH: 1156
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-09-661-322A-28

Query Match 7.4%; Score 62.5; DB 5; Length 1156;
Best Local Similarity 26.0%; Pred. No. 43;
Matches 39; Conservative 18; Mismatches 48; Indels 45; Gaps 9;

QY 21 VPPSNLEGSQSDERALLD--QLHTLLSNTDATGLEIDRA-LGIPELVN-----OGAL 71
DB 912 VGP--LSEGESIERORONAKMKNMELGRRRA---EIDRVYLAQAQAINHFLVDYQDOL 964
QY 72 EPKODAFGGGEAAVMDQKAGLYGOT-----YPAOGPPMOGFGHLOG-----OS 115
DB 965 NPEIGLAEINERNSLVESISGYSTLLOIGPINEITYTEISDRLOQASVLTSSNAVON 1024
QY 116 PSFNSMNMNM-----OQGNFPLOGMH 137
DB 1025 GDFNSGLDSMNTMDASVQODCN-----MH 1049

RESULT 8
US-09-739-449-10802
Sequence 10802, Application US/09739449

GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 10802
LENGTH: 181
TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-09-739-449-10802

Query Match 7.3%; Score 62; DB 5; Length 181;
Best Local Similarity 32.6%; Pred. No. 4.3;
Matches 28; Conservative 12; Mismatches 30; Indels 16; Gaps 5;

QY 14 RNSLDLVGPPSNLEGSQSDERALLD--QLHTLL--SNTDATGLEIDRALGIPELVNO 67
DB 31 RQCLTEALG--NLGEPDLSLLTDMQSRSLDLKHSNGSARSISIKWIDRA---AVLICR 84
QY 68 GQALEPKODAFGGGEAAVMDQKAGL 93
DB 85 DYLENSADFTVVSQE---LEQISGL 106

RESULT 9
US-09-819-142-24
Sequence 24, Application US/09819142
GENERAL INFORMATION:
APPLICANT: Reuber, Lynne
APPLICANT: Ratcliffe, Oliver
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Riechmann, Jose Luis
APPLICANT: Heard, Jacqueline
TITLE OF INVENTION: Methods for Modifying Flowering Phenotypes
FILE OF INVENTION: MBI-0033
FILE REFERENCE: MBI-0033
CURRENT APPLICATION NUMBER: US/09/819,142
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
LENGTH: 669
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-819-142-24

Query Match 7.3%; Score 62; DB 5; Length 669;
Best Local Similarity 24.4%; Pred. No. 24;
Matches 49; Conservative 22; Mismatches 70; Indels 60; Gaps 13;

QY 7 TQNRPLRNSL---DDLVPSPSNLEGSQSDERALLDQLHTLLSNTDATGLEIDRA-LGI 61
DB 299 SOHGNLNNSEFTGQDAFGLSTLNG-FDLQAL-----AVTGQLPAQSLAQQAAGIGR 352
QY 62 PELVNOG---QALEPKODAFGGGEAAVMDQKAGLYGQTPPAOGPPMOGFGH-----LQ 112
DB 353 PAMWSKGLPVSSIVDERSTFSFNTKTRFEGELGHQO-QPQOPQW-NLHGVPTGLQ 410
QY 113 GQSPFNSMNMNM-----OQGN-----FPLOGMH--PR-----ANIMRP--- 145
DB 411 QQLPWGNRMSIQOQIAAAYRAAGNSVYNNGMPLPAGQOQSLPRGPPMLTSSQSSIRQPMLS 470
QY 146 -----RTNTPKQLRM 155
DB 471 NRISERSGSGRRNNIPRESSRV 491

DB 517 KSKKPGSVKTERAGAGQ-IEKOMVVRGGRVGRGRGP-VNLAVLKLSHOG 565

RESULT 14

US-09-739-449-13145
; Sequence 13145, Application US/09739449
; GENERAL INFORMATION:

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15490)C

; CURRENT APPLICATION NUMBER: US/09/739,449

; PRIOR FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: US 09/514,000

; NUMBER OF SEQ ID NOS: 13351

; SEQ ID NO 13145

; LENGTH: 365

; TYPE: PRT

; ORGANISM: Agrobacterium tumefaciens

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(365)

; OTHER INFORMATION: unsure at all Xaa locations

US-09-739-449-13145

Query Match 7.0%; Score 59; DB 5; Length 365;

Best Local Similarity 20.6%; Pred. No. 21;

Matches 34; Conservative 24; Mismatches 49; Indels 58; Gaps 8;

OY 19 DIVGPPSNLEGO-----SDERALDOLHTLSN--TDATGLEIDRALGIPE 63

DB 133 DVKAPISGIVGARITREGALVATSGSENLATIQOLDPIADFTQPRADIRLKLAL---- 188

OY 64 LVNQGSALEPKODAFQGOEAAVMDQKAGLYGQYPPAGPPOGPFHLOGQSPFSNMN 123

DB 189 --QDCQLMTGQNEA---EVNLLFDD---GSRYPVSG-----RLTFSEAAVDETTG 230

OY 124 QMNQGNFP-----LQGHPRANIMRPRNTNPKOLRMOLQRLQ 162

DB 231 QVTLRGEFPNPGDILPGMY-----VRVQIQOQIQ 260

RESULT 15

US-09-739-449-11226
; Sequence 11226, Application US/09739449
; GENERAL INFORMATION:

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15490)C

; CURRENT APPLICATION NUMBER: US/09/739,449

; PRIOR FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: US 09/514,000

; NUMBER OF SEQ ID NOS: 13351

; SEQ ID NO 11226

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Agrobacterium tumefaciens

US-09-739-449-11226

Query Match 6.9%; Score 58.5; DB 5; Length 306;

Best Local Similarity 23.9%; Pred. No. 19;

Matches 28; Conservative 12; Mismatches 34; Indels 43; Gaps 5;

OY 23 PSNLEG--QSDERALDOLHTLSN-----DATGLEIDR--ALGIPELVNQGAL 71

DB 96 PLSNIDALRALDMRIELTNLHRTKATMTYVTHDOVEAMTMADRIYVLNAGEIAOVGAPL 155

OY 72 E-----PKOD-----AFQGOEAAVMDQKAGLYGQ 96

DB 156 ELYHRRPANTFVAGFIGNPKMFLKVTCKSVSAEGVTVAVEGQITIVPVEPRAGLEBK 212

Search completed: April 19, 2001, 16:54:13
Job time: 497 sec

